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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:07:04 ; Search time 23 seconds
(without alignments)
425.383 Million cell updates/sec

Title: US-10-024-433-2
1264

Perfect score: 1 MTGFEARLIFGTWMSYVK.....VDRCPMSAVIDKRVFMS 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1264	100.0	236	BIR8_HUMAN	Q96P09 homo sapien
2	1241	98.2	236	BIR8_PANTR	Q95M72 pan troglod
3	1237	97.9	236	BIR8_GORGO	Q95M71 gorilla gor
4	1052	83.2	497	BIR4_HUMAN	P98170 homo sapien
5	1029	81.4	496	BIR4_RAT	Q9016 ratu mus norv
6	1028	81.3	496	BIR4_MOUSE	Q60989 mus musculu
7	472.5	37.4	604	BIR2_HUMAN	Q13489 homo sapien
8	458.5	36.3	618	BIR3_HUMAN	Q13480 homo sapien
9	455.5	36.0	600	BIR3_MOUSE	Q08863 mus musculu
10	454.5	36.0	611	BIR3_CHICK	Q90660 gallu galli
11	443	35.0	612	BIR3_MOUSE	Q92210 mus musculu
12	427	33.8	358	PIAP_PIG	Q62640 sus scrofa
13	401	31.7	498	IAP2_DROME	Q24307 drosophila
14	373.5	29.5	298	BIR7_HUMAN	Q96C85 homo sapien
15	335	26.5	438	IAP1_DROME	Q24306 drosophila
16	314.5	24.9	275	IAP1_GVCP	P41437 oryza pomon
17	312.5	24.7	268	IAP3_NPYOP	Q9016 mus musculu
18	228.5	18.1	1403	BIRE_MOUSE	Q9146 mus musculu
19	223.5	17.7	1403	BIRE_MOUSE	Q9143 mus musculu
20	222.5	17.6	1402	BIR6_MOUSE	Q9143 mus musculu
21	222.5	17.6	1447	BIR6_MOUSE	Q9143 mus musculu
22	218.5	17.3	1403	BIRA_MOUSE	Q90W5 mus musculu
23	209.5	16.6	1403	BIR1_HUMAN	Q13075 homo sapien
24	206.5	16.3	239	ZFP_IRV6	P47732 chilo litide
25	184	14.6	286	IAP1_NPYOP	P41435 autographa
26	182	14.4	275	IAP1_NPYOP	Q10266 oryza pseu
27	165.5	13.1	249	IAP2_NPYOP	P41434 autographa
28	134	10.6	142	BIR5_RAT	Q9147 ratu mus norv
29	132	10.4	140	BIR5_MOUSE	Q70201 mus musculu
30	130	10.3	142	BIR5_HUMAN	Q15392 homo sapien
31	127.5	10.1	4829	BIR6_HUMAN	Q90R99 homo sapien
32	126	10.0	145	ZFP_IRV6	P40639 chilo litide
33	111	8.8	433	RN26_HUMAN	Q9BY88 homo sapien

34	109.5	8.7	489	MDM4_MOUSE	O35618 mus musculu
35	108	8.5	487	MDM2_CANFA	P56950 canis fam11
36	106.5	8.4	224	IAPL_ASPM1	O11452 african swi
37	104.5	8.3	224	IAPL_ASPB7	O65138 african swi
38	104.5	8.3	490	MDM4_HUMAN	O15151 homo sapien
39	104	8.2	491	MDM2_HORSE	P56951 equus cabal
40	102	8.1	236	IAP2_NPYOP	O10324 oryza pseu
41	100.5	8.0	224	IAPL_ASPFH	O12407 african swi
42	98	7.8	473	MDM2_XENLA	P56273 xenopus lae
43	98	7.8	539	MDM2_HUMAN	O12899 homo sapien
44	96.5	7.6	224	IAPL_ASPC3	O11451 african swi
45	96	7.6	491	MDM2_HUMAN	Q00987 homo sapien

ALIGNMENTS

RESULT 1
BIR8_HUMAN
ID BIR8_HUMAN STANDARD: PRT; 236 AA.
AC Q96P09: Q96RMS; 236
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
DE like protein 2) (IAP-like protein 2) (ILP-2) (Testis-specific
DE inhibitor of apoptosis).
GN BIR8 OR ILP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX PubMed=11597143;
RA Lagace M., Xuan J.-Y., Young S.S., McRoberts C., Maier J.,
RA Rajcan-Separovic E., Korneluk R.G.;
RT "Genomic organization of the X-linked inhibitor of apoptosis and
RT identification of a novel testis-specific transcript.";
RL Genomics 77:181-186(2001).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Refey S.B.,
RA Frittlin A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezzone P., Pearnhead H.O., Duckett C.S.;
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RT Mol. Cell. Biol. 21:4292-4301(2001).
CC - FUNCTION: Protects against apoptosis mediated by BAX.
CC - SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC - SUBUNIT: Binds to caspase-9.
CC - TISSUE SPECIFICITY: Testis-specific in normal tissues.
CC - SIMILARITY: BELONGS TO THE IAP FAMILY.
CC - SIMILARITY: CONTAINS 1 BIR REPEAT.
CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

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CC EMBL, AF420440; AAL30369.1; -
CC EMBL, AF164682; AAK81892.1; -
CC Genbank, HGNC:14878; BIR8.
CC InterPro: IPR001370; BIR.
CC InterPro: IPR001841; Znf_rlng.
CC Pfam: PF00653; BIR; 1.
CC Pfam: PF00097; zf-C3HC4; 1.

DR PROSITE: PS01282; BIR_REPEAT_1; 1.
 DR PROSITE: PS0143; BIR_REPEAT_2; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS0089; ZF_RING_2; 1.
 KW Apoptosis; Zinc-finger.
 FT REPEAT 70 BIR.
 FT ZN_FING 189 224 RING-TYPE.
 FT CONFLICT 196 196 Y->H (IN REF. 2).
 SQ SEQUENCE 236 AA; 27115 MM; CB7F034BDDDFAD9D CRC64.

Query Match 100.0%; Score 1264; DB 1; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.3e-94;
 Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGEARLITFGTWMYVYNKEQLARAGFYALGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
 DB 1 MTGEARLITFGTWMYVYNKEQLARAGFYALGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
 QY 61 KWPFGCKYLLEEKHEYNINHLRSLGALVQTTKTPSLTKRISDTIFPNMLOEAI 120
 DB 61 KWPFGCKYLLEEKHEYNINHLRSLGALVQTTKTPSLTKRISDTIFPNMLOEAI 120
 QY 121 MGFDFKVKKIMEERIQSGSNKYKLEVLVADLVSAQKDTENELNQTSLQREISPEPL 180
 DB 121 MGFDFKVKKIMEERIQSGSNKYKLEVLVADLVSAQKDTENELNQTSLQREISPEPL 180
 QY 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTKQCAEAVDRCPMCSAVIDEKORVEMS 236
 DB 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTKQCAEAVDRCPMCSAVIDEKORVEMS 236

RESULT 2

BIR8_PANTR STANDARD; PRT; 236 AA.

ID BIR8_PANTR STANDARD; PRT; 236 AA.
 AC Q95M72;
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
 like protein 2) (IAP-like protein 2) (ILP-2).
 GN BIRC8 OR ILP2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OX NCBI_TaxID=9595;
 RN [1]
 RP MEDLINE=21286921; PubMed=11390657;
 RA Richter B.W.M., Mir S.S., Eiden L.J., Lewis J., Refey S.B.,
 RA Fratini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
 RA Notarangelo L.D., Vezoni P., Fearhead H.O., Duckett C.S.;
 RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
 apoptosis protein family.";
 RT Mol. Cell. Biol. 21:4292-4301(2001).
 RL Mol. Cell. Biol. 21:4292-4301(2001).
 CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SUBUNIT: Binds to caspase-9 (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BIR_REPEAT.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL: AY030052; AAK49776.1; -;
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001841; Znf_fing.

DR Pfam; PF00653; BIR; 1.
 DR Pfam; PF00097; ZF_C3HC4; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 1.
 DR PROSITE: PS0143; BIR_REPEAT_2; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS0089; ZF_RING_2; 1.
 KW Apoptosis; Zinc-finger.
 FT REPEAT 70 BIR.
 FT ZN_FING 189 224 RING-TYPE.
 SQ SEQUENCE 236 AA; 27136 MM; 64CCA3A251420EDE CRC64;

Query Match 98.2%; Score 1241; DB 1; Length 236;
 Best Local Similarity 97.9%; Pred. No. 9e-93;
 Matches 231; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTGEARLITFGTWMYVYNKEQLARAGFYALGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
 DB 1 MTGEARLITFGTWMYVYNKEQLARAGFYALGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
 QY 61 KWPFGCKYLLEEKHEYNINHLRSLGALVQTTKTPSLTKRISDTIFPNMLOEAI 120
 DB 61 KWPFGCKYLLEEKHEYNINHLRSLGALVQTTKTPSLTKRISDTIFPNMLOEAI 120
 QY 121 MGFDFKVKKIMEERIQSGSNKYKLEVLVADLVSAQKDTENELNQTSLQREISPEPL 180
 DB 121 MGFDFKVKKIMEERIQSGSNKYKLEVLVADLVSAQKDTENELNQTSLQREISPEPL 180
 QY 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTKQCAEAVDRCPMCSAVIDEKORVEMS 236
 DB 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTKQCAEAVDRCPMCSAVIDEKORVEMS 236

RESULT 3

BIR8_GORGO STANDARD; PRT; 236 AA.

ID BIR8_GORGO STANDARD; PRT; 236 AA.
 AC Q95M71;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-
 like protein 2) (IAP-like protein 2) (ILP-2).
 GN BIRC8 OR ILP2.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
 OX NCBI_TaxID=9595;
 RN [1]
 RP MEDLINE=21286921; PubMed=11390657;
 RA Richter B.W.M., Mir S.S., Eiden L.J., Lewis J., Refey S.B.,
 RA Fratini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
 RA Notarangelo L.D., Vezoni P., Fearhead H.O., Duckett C.S.;
 RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
 apoptosis protein family.";
 RT Mol. Cell. Biol. 21:4292-4301(2001).
 RL Mol. Cell. Biol. 21:4292-4301(2001).
 CC -1- FUNCTION: Protects against apoptosis mediated by BAX (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SUBUNIT: Binds to caspase-9 (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BIR_REPEAT.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL: AY030053; AAK49777.1; -;
 DR InterPro: IPR001370; BIR.


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FT REPEAT      26          93       BIR 1.
FT REPEAT     163         230       BIR 2.
FT REPEAT     264         329       BIR 3.
FT ZN_FING    449         484       RING-TYPE.
SQ SEQUENCE   496 AA; 56072 MW; E250E3C7461A469 CRC64;

Query Match
Best Local Similarity 76.7%; Score 1029; DB 1; Length 496;
Matches 181; Conservative 33; Mismatches 22; Indels 0; Gaps 0

QY 1 MTGYEARLITFGTWMYSVYNKEOLARAGFAFIAIQEDKVKCFHGGGGLANMKPKEDPEECHA 60
DB 261 MAEYDARIYFTGTWLYSVNKEQLARAGFAFALBEGSKVKCFHGGGGLTDMPEDPEECHA 320
QY 61 KRYPCCKYLLEKGHEHYINNIHLTSLBSALAVQTTRKPSLTFRISDTIFPNPMQEAIR 120
DB 321 KMYPCCKYLLEDKGGEYINNIHLTSLGSBYRAETKPSPVTKKIDDTIFQNPMVOEAIR 380
QY 121 MGDFPRDYAKRIEEKRTSGSNKYKTLEYVADLVASOKOTTEINLOTLSLOREISPEPL 180
DB 381 MGFNRKDIDIKTMEEKLQTSNGSYLSLEVLIADLVASOKDNDSDESSQSLQDISTEEOL 440
QY 181 RLQOEELCKICMDRYIAVFIPCGHLTYTCOCAEAYVDRCMCAVAVIDFKRQVFNFS 236
DB 441 RLQOEELCKICMDRNIAIVFPVGCHLYTCOCAEAYVDRCMCAVAVIDFKRQVFNFS 496

RESULT 6
BIR4_MOUSE
ID BIR4_MOUSE STANDARD; PRT; 496 AA.
AC Q60989; 008865;
DT 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis
DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
DE BIRC4 OR API3 OR XIAP OR MIR4.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RL [1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RC MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors".
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RN SEQUENCE FROM N.A.
RP Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/CDNJ databases.
CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
CC (by similarity).
CC -1- SUBUNIT: Interacts with SMAC and with PRS525; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3
CC and -7, while the third BIR is involved in caspase-9 inhibition.
CC The interactions with SMAC and PRS525 are mediated by the second
CC and third BIR domains (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
 DR EMBL: U36842; AAC52594.1; -
 DR EMBL: U88990; AAB58376.1; -
 DR HSSP: Q13490; 10BH.
 DR MGD; MGI:107572; BIRCA.
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF00653; BIR; 3.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS0143; BIR_REPEAT_2; 3.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KM Apoptosis; Zinc-finger; Repeat.
 FT REPEAT 26 93 BIR 1.
 FT REPEAT 163 230 BIR 2.
 FT REPEAT 264 329 BIR 3.
 FT ZN_FING 449 484 RING-TYPE.
 FT CONFLICT 208 208 E -> K (IN REF. 2).
 FT CONFLICT 317 317 E -> D (IN REF. 2).
 FT CONFLICT 322 322 W -> C (IN REF. 2).
 FT CONFLICT 346 346 S -> P (IN REF. 2).
 FT CONFLICT 360 360 S -> P (IN REF. 2).
 FT CONFLICT 388 388 I -> L (IN REF. 2).
 FT CONFLICT 449 449 C -> S (IN REF. 2).
 FT CONFLICT 462 462 V -> F (IN REF. 2).
 FT CONFLICT 468 468 V -> A (IN REF. 2).
 FT CONFLICT 490 490 K -> N (IN REF. 2).
 SQ SEQUENCE 496 AA; 56079 MW; ECSFAE0799F2CDD8 CRC64;
 Query Match 81.3%; Score 1028; DB 1; Length 496;
 Best Local Similarity 78.4%; Pred. No. 2.7e-75;
 Matches 185; Conservative 26; Mismatches 25; Indels 0; Gaps 0;
 QY 1 MTGPEARLITGTYWYSVKNKEDLARAAGFYAIOEDKVCFFHGGGLANMKPKEDPEQHA 60
 DB 261 MAEYEARIVTGTGTSVSKEDLARAAGFYALDEGKVCFFHGGGLTDMKPSDPEQHA 320
 QY 61 KMYGCKKLLDEKGEYINNIHLTSLREGALVQTTRKPSLTKRIDTFFPMLEAIR 120
 DB 321 KMYGCKKLLDEKGEYINNIHLTSLREGALVQTTRKPSLTKRIDTFFPMLEAIR 380
 QY 121 MGDFDKVAKIMEIRIQTSGSNYKLEVLADLVSAQKDTENELNQTSLQREISPEPL 180
 DB 381 MGDFDKVAKIMEIRIQTSGSNYKLEVLADLVSAQKDTENELNQTSLQREISPEPL 440
 QY 181 RLQDEKICKCMQRYIVAFIPCGHLYVCKQCAEAVDRCPCSAVIDFKORVEM 236
 DB 441 RLQDEKICKCMQRYIVAFIPCGHLYVCKQCAEAVDRCPCSAVIDFKORVEM 496
 RESULT 7
 BIR2_HUMAN STANDARD: PRT; 604 AA.
 ID BIR2_HUMAN Q13489; Q13489; Q9UP46; Q9HC27;
 AC Q13489; Q13489; Q9UP46; Q9HC27;
 DT 01-NOV-1997 (rel. 35; Last sequence update)
 DT 01-NOV-1997 (rel. 35; Last sequence update)
 DT 15-JUN-2002 (rel. 41; Last annotation update)
 DE Baculoviral iAP repeat-containing protein 1 (Inhibitor of apoptosis protein 1) (HiAP1) (HiAP-1) (C-IAP2) (TNFR2-TRAF signaling complex protein 1) (IAP homolog C).
 GN BIR2 OR API OR IAP1 OR MHC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96128127; PubMed=8548810;

RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
 RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";
 RL Cell 83:1243-1252(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96149249; PubMed=8552191;
 RA Liston P., Roy N., Tanai K., Lefebvre C., Baird S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related family of iAP genes.";
 RL Nature 379:349-353(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=96209843; PubMed=8643514;
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls R.L., Vaux D.L.;
 RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99252096; PubMed=10233894;
 RA Horrevoets A.J., Fontijn R.D., Van Zonneveld A.J., de Vries C.J., ten Cate J.W., Pannekoek H.;
 RT "Vascular endothelial genes that are responsive to tumor necrosis factor-alpha in vitro are expressed in atherosclerotic lesions, including inhibitor of apoptosis protein-1, stannin, and two novel genes.";
 RL Blood 93:3418-3431(1999).
 RN [5]
 RP SEQUENCE OF 362-441 FROM N.A.
 RX MEDLINE=20519161; PubMed=11066071;
 RA Beens M., Steyts A., Dierlam J., De Wolf-Peters C., Marynen P.;
 RT "Structure of the M17 gene and molecular characterization of the B-cell lymphomas of MALT type.";
 RL Genes Chromosomes Cancer 29:281-291(2000).
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES, INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
 CC -1- DISEASE: Involved in a t(11;18)(q21;q21) chromosomal translocation recurrent in low-grade MALT lymphoma (Mucosa-associated lymphoid tissue). This translocation is found in approximately 50% of cytogenetically abnormal low-grade MALT lymphoma and involves MALTI and BIRC2.
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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DR PDB; 1QBH; 20-OCT-99.
 DR Genew; HGNC:590; BIRC2.
 DR MIM; 601721; -.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00653; BIR; 3.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS30089; ZF_RING_2; 1.
 DR Apoptosis; Zinc-finger; Repeat; 3D-structure.
 KW REPEAT 46 113 BIR 1.
 FT REPEAT 184 250 BIR 2.
 FT REPEAT 269 336 BIR 3.
 FT DOMAIN 453 543 CARD.
 FT ZN_FING 571 606 RING-TYPE.
 FT CONFLICT 157 157 S -> P (IN REF. 2).
 FT CONFLICT 308 308 C -> G (IN REF. 2).
 FT CONFLICT 414 414 Q -> L (IN REF. 2).
 FT CONFLICT 514 514 L -> W (IN REF. 2).
 SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Query Match 36.3%; Score 458.5; DB 1; Length 618;
 Best Local Similarity 29.5%; Pred. No. 1.9e-29;
 Matches 104; Conservative 50; Mismatches 82; Indels 117; Gaps 6;

QY 1 MTGEARLITFGTMYM--VAKEDLARGFAIGEDKVDYVCGGGLANMKPKEDPMQ 58
 | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
 DB 266 MQTHAARIRTFMYPSSVVPQEDLASAGFYVGRNDYKCCFCGGLCWESGDDPWE 325
 59 HAKWPGCKYLLEKGEHYINNI-----HLRSLGALVQTKKT-----PSLTKR 104
 ||||| : : : | : : : | : : : | : : : | : : : | : : : | : : :
 DB 326 HAKWPGCEYLRLKRGEPFVSQVAGYPHLEQLSTSDTGEENADPPIHFGGESS 385
 105 ISDTIFPNMLQEAIRMGDFDKVKKIMEERIQTSNGSNYKTELVADVSAQKDTENE 164
 :
 DB 386 EDAYMNTPVYKSALEMGFNDLVQYVQSILTTGENYKTVNDIVSALLNEDEREKE 445
 165 -----LNQTSIQ 171
 DB 446 KEKQAEEMASDLSLRKRNALFQQLTCVLPILDNLKANYINKQEHDIKQTKQIPQ 505
 172 -RE-----ISPEPLRL 183
 || :
 DB 506 ARELIDITLVKGNAAANFRKNCLEIDSTLYKNLFVDKMKYIPEEDVSGLSLEOLRL 565
 184 QEEKICRICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMSAVIDKQRFVMS 236
 ||| :
 DB 566 QEERTKVCMDKEVSVFIPCGHLVTCQCAEAPSLKPCICRGIINGVTFTLS 618

RESULT 9
 BIR2_MOUSE
 ID BIR2_MOUSE STANDARD; PRT; 600 AA.
 AC 008863;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 13-JUN-2002 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis protein 1) (MIAP1) (MIAP-1).
 GN BIRC2 OR API1 OR IAP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=skeletal muscle;
 RX MEDLINE=98110590; PubMed=9441758;
 RA Liston P., Lefevre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
 RT "Genomic characterization of the mouse inhibitor of apoptosis protein 1 and 2 genes."
 RL Genomics 46:495-503(1997).
 CC - FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
 CC - SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity (BY SIMILARITY).
 CC - SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC - SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC - SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC - SIMILARITY: CONTAINS 1 CARD DOMAIN.
 CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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 CC -----

DR EMBL; U88908; AAC53531.1; -.
 DR HSSP; Q13490; 1QBH.
 DR MGD; MG1:1197007; Birc2.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00653; BIR; 3.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 DR Apoptosis; Zinc-finger; Repeat.
 KW REPEAT 27 94 BIR 1.
 FT REPEAT 167 233 BIR 2.
 FT REPEAT 253 320 BIR 3.
 FT DOMAIN 436 525 CARD.
 FT ZN_FING 553 588 RING-TYPE.
 SQ SEQUENCE 600 AA; 67198 MW; AD7F73E6849317D1 CRC64;

Query Match 36.0%; Score 455.5; DB 1; Length 600;
 Best Local Similarity 28.9%; Pred. No. 3.2e-29;
 Matches 103; Conservative 48; Mismatches 80; Indels 125; Gaps 8;

QY 1 MTGEARLITFGTMYM--VAKEDLARGFAIGEDKVDYVCGGGLANMKPKEDPMQ 58
 | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
 DB 250 MQTHAARIRTFMYPSSVVPQEDLASAGFYVGRNDYKCCFCGGLCWESGDDPWE 309
 59 HAKWPGCKYLLEKGEHYINNI-----HLRSL-----EGALVQTKTKTPTSL 101
 ||||| : : : | : : : | : : : | : : : | : : : | : : : | : : :
 DB 310 HAKWPGCEYLRLKRGEPFVSQVAGYPHLEQLSTSDTGEENADPPIHFGGESS- 368
 102 TKRISDTI-FPNMLQEAIRMGDFDKVKKIMEERIQTSNGSNYKTELVADVSAQKDT 160
 :
 DB 369 -----EDVVMSTPVYKSALEMGFNSLRVQVQQLIATGENYKTVNDIVSALLNEDEREKE 424
 161 TENELND----- 167
 || :
 DB 425 RESQMEQAEEMASDLSLRKRNALFQQLTCVLPILDNLKANYINKQEHDIKQTKQIPQ 484
 168 -----TSLQ-----REISP-----EBPL 180


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CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
DR EMBL: I49433; AAC42078.1; -
DR EMBL: U98909; AAC53532.1; -
DR HSSP: Q13490; 10BH.
DR MGD: MG1:1197009; BIRC3.
DR Interpro: IPR001370; BIR.
DR Interpro: IPR001315; CARD.
DR Interpro: IPR001841; Znf.fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat.
DR REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_FING 565 600 RING-TYPE.
FT CONFLICT 380 380 E -> K (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match 35.0%; Score 443; DB 1; Length 612;
Best Local Similarity 28.8%; Pred. No. 3.3e-28;
Matches 104; Conservative 49; Mismatches 76; Indels 132; Gaps 8;

QY 1 MTGEARLITFGTMYW--VNKEOLARAGFYAIGQEDKOCFHCGGLANMKPKEDPWEQ 58
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 259 MCHSAALRTFLYKPPSPVQPEQLASGFIYVDRNDYKCCGCCGGLKCMWEPGDDPWLE 318
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 59 HAKWYPCCKYLLEKRGHEYNIN--HLRSLGALVQTTKTPSLTKRISD----- 107
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 319 HAKWFPCEFLIRKGFQFVDEIQARYPHLEQL-----LSTSDTPG--EENADPTETV 371
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 108 -----TIFPNMLOAIRMGFDFKDYKIMERIQTSGSNYKTLLEVADLVSA 156
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 372 HFGPGESEEDVVMSTPVYKAALEMGFSRSLVROTVOQLIATGENYRTVNDIVSVLNA 431
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 157 OKOTTENE-----IS 175
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 432 EDERREBEKERQTEMASGDSLIRKNMALFQQLTHVLPILDNLEASVITKQEHDIIR 491
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 165 -LNQTSIQ-RE----- 164
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 492 OKTOIPLOARELIDTVLVKNAANIFKNSLKEIDSTIYENLFVEKNMXYIPTEDEVSGLS 551
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 176 PEEPLRLQOEKLIKICMDRYIAVFEPCGHLYMKQCEANADRCMCAVDFKRVAM 235
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 552 LEEPLRLQOEKLIKICMDRYIAVFEPCGHLYMKQCEANADRCMCAVDFKRVAM 235
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 236 S 236
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 612 S 612

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PIAP_PIG
ID PIAP_PIG STANDARD; PRT; 358 AA.
AC 062640;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative inhibitor of apoptosis.
GN PIAP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
ON NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98162622; Pubmed=9501011;
RA Stehlik C., de Martin R., Binder B.R., Lipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis
RL protein (Iap) family member is regulated by NF-kappa B.";
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U79142; AAC39171.1; -
DR HSSP: Q13490; 10BH.
DR Interpro: IPR001370; BIR.
DR Interpro: IPR001315; CARD.
DR Interpro: IPR001841; Znf.fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Apoptosis; zinc-finger; Repeat.
DR REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT DOMAIN 193 283 CARD.
FT ZN_FING 311 346 RING-TYPE.
SQ SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;

Query Match 33.8%; Score 427; DB 1; Length 358;
Best Local Similarity 34.3%; Pred. No. 3.3e-27;
Matches 96; Conservative 45; Mismatches 87; Indels 52; Gaps 8;

QY 1 MTGEARLITFGTMYW--VNKEOLARAGFYAIGQEDKOCFHCGGLANMKPKEDPWEQ 58
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 87 MGYAARFKTFCKMNPSSIPVHPPEQLASGFIYMGHSDVCKCCGCCGGLKCMWEPGDDPWLE 146
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 59 HAKWYPCCKYLLEKRGHEYNIN--HLRSLGALVQTTKTP-----SLT 102
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 147 HAKWFPCEFLIRKGFQFVDEIQARYPHLEQL-----LSTSDNPEDENAEPNDLSLI 201
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 103 KRISDTIFPN-----PMLOAIRMGFDFKDYKIMERIQTSGSNYKTLLEVADLVSAQ 157
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 202 RKNMALFQQLTHVLPILDNLEASVITKQEHDIIR-----LVKGN 258
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 158 KDTT--ENELNQ-----TSLOREISPEEPLRLQOEKLIKICMDRY 196

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DB 259 YAAITIKNSIQEIDPMYKHLFWOODIKYIPTEVNSDLSMEQJRLQDEFTCKVCMKE 318
 QY 197 IAWFIPCGHLYTCOCAGAVDRCPMCSANVDFKORVEMS 236
 DB 319 VSVIFPCGHLVYCKOCAPSLRRCPIRGITKGVRTLS 358

RESULT 13
 IAP2.DROME STANDARD: PRT: 498 AA.
 AC 024307: 024177; 024115; 024149; Q9V7G1;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apoptosis 2 inhibitor (inhibitor of apoptosis 2) (DIAP2) (DIAP) (IAP
 homolog A) (IAP-like protein) (DILP).
 GN IAP2 OR ILP OR DIHA OR CG8293.
 OS Drosophila melanogaster (Fruit fly)
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye; imaginal disk.
 RX MEDLINE=96128128; PubMed=8548811;
 RA Hay B.A., Wassarman D.A., Rubin G.M.;
 RT "Drosophila homologs of baculovirus inhibitor of apoptosis proteins
 function to block cell death."
 RL Cell 83:1253-1262(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=96149249; PubMed=8552191;
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertont-Horvat G.,
 RA Farhan R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related
 family of IAP genes."
 RL Nature 379:349-353(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=96256286; PubMed=8654366;
 RA Duckett C.S., Nawa V.E., Gedrich R.W., Clem R.J., van Dongen J.L.,
 RA Gilliland M.C., Shieles H., Hardwick J.M., Thompson C.B.;
 RT "A conserved family of cellular genes related to the baculovirus Iap
 gene and encoding apoptosis inhibitors."
 RL EMBO J. 15:2685-2694(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RA Ross J.L.;
 RL Thesis (1991), Vanderbilt University / Nashville, U.S.A.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Gelinkler S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies A.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Krait C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Ruskern D.R., Paclet J.M.,
 RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Slater E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytkas R., Tector C., Turner C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [6]
 RP SEQUENCE OF 17-498 FROM N.A.
 RC TISSUE=Larva;
 RX MEDLINE=96209843; PubMed=8643514;
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
 RT "Cloning and expression of apoptosis inhibitory protein homologs that
 function to inhibit apoptosis and/or bind tumor necrosis factor
 receptor-associated factors."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
 CC -I- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND
 CC HID-DEPENDENT CELL DEATH IN THE EYE.
 CC -I- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS THROUGHOUT
 CC DEVELOPMENT.
 CC -I- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -I- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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 CC -----
 DR EMBL: LA9441; AAC41610.1; -;
 DR EMBL: U45881; AAC45988.1; -;
 DR EMBL: U43733; AAC47155.1; -;
 DR EMBL: M96581; -; NOT_ANNOTATED_CDS.
 DR EMBL: AE003809; AAF58095.1; -;
 DR EMBL: U38809; AAB08398.1; -;
 DR HSSP: Q13490; IOBH.
 DR Flybase: FBgn015247; Iap2.
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001841; zif_Ring.
 DR Pfam: PF00097; zif-C3HC4; 1.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 3.
 DR PROSITE: PS0143; BIR_REPEAT_2; 3.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS00089; ZF_RING_2; 1.
 KW Apoptosis; zinc-finger; Repeat.
 FT REPEAT 9 76
 FT REPEAT 113 179
 FT REPEAT 212 279
 FT ZN_FING 451 486
 FT CONFLICT 5 5
 FT CONFLICT 40 40
 FT N -> K (IN REF. 2).

FT CONFLICT 64 65 ER -> AG (IN REF. 3).
 FT CONFLICT 94 94 A -> K (IN REF. 1).
 FT CONFLICT 282 282 A -> D (IN REF. 6).
 FT CONFLICT 286 286 A -> S (IN REF. 3).
 FT CONFLICT 302 302 P -> Q (IN REF. 2 AND 5).
 FT CONFLICT 303 303 P -> T (IN REF. 6).
 FT CONFLICT 327 327 A -> T (IN REF. 2).
 FT CONFLICT 369 376 ALEVRP -> DMRCASR (IN REF. 3).
 SQ SEQUENCE 498 AA; 54506 MW; 66EC36DA6ED2AD6 CRC64;
 Query Match 31.7%; Score 401; DB 1; Length 498;
 Best Local Similarity 30.8%; Pred. No. 6e-25;
 Matches 89; Conservative 46; Mismatches 94; Indels 60; Gaps 4;
 QY 5 EARLITGTMTYS--VNKEQLARAGFYAIGQEDKYQCHCGGLANWKREKPEWQHAW 62
 DB 213 DARIETPTDPIISINOPASALAGLYQKIGDQYRCHCNIGLSWQKDEPWEHAW 272
 QY 63 YPGCKYLLEEGHYINNIHLRSLGALVQTKTPSLTKRISPTIFPNMLQEAIRMG 122
 DB 273 SPKQFVILAKGPAVSEVLTATMANASSPATAPITQ---ADYIMDEAPAKELALG 329
 QY 123 FDFKDKKIMEERIQTSGSNKTEVL----- 149
 DB 330 IDGGVVRNAIQKRLISSGCAFSSTLDELHIDPDAGAGALEVRPEPSPAFTEPCQAT 389
 QY 150 -----VADYSAQKDTTENLNOTSLQREI-----SPEEPLRLQDEK 187
 DB 390 TSKASAVIPYADSTIPAKPQAAEAVANISKITDELQKMSVAPNGLSLEEKRLQKAR 449
 QY 188 LCKICIMRYIAVFIPIGCHLYTCQCAVDRCPMCASAVIDKQRYEWS 236
 DB 450 LCKYCLDEBVGVLPCGHLATCNCQCAPSVANCPMCRAIDIKGVRFFLS 498
 RESULT 14
 BIR7_HUMAN STANDARD; PRT; 298 AA.
 ID BIR7_HUMAN
 AC 096CA5; 09H2A8; 09H0V0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 7 (Kidney inhibitor of apoptosis protein) (KIAP) (Melanoma inhibitor of apoptosis protein) (MI-IAP) (Livin).
 DE BIRC7 OR KIAP OR MLTAP OR LIVIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fetal Kidney;
 RX PubMed=11162435;
 RA Lin J.-H., Deng G., Huang Q., Morser J.;
 RT "KIAP, a novel member of the inhibitor of apoptosis protein family.";
 RL Biochem. Biophys. Res. Commun. 279:820-831(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Melanoma;
 RX PubMed=11322947;
 RA Ashnab Y., Allan A., Pollack A., Panet A., Yehuda D.B.;
 RT "Two splicing variants of a new inhibitor of apoptosis gene with different biological properties and tissue distribution pattern.";
 RL PEBB Lett. 495:56-60(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Kidney;
 RX PubMed=11024045;
 RA Kasof G.M., Gomes B.C.;
 RT "Livin, a novel inhibitor of apoptosis protein family member.";
 RL J. Biol. Chem. 276:3238-3246(2001).
 RN [4]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deacon R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle P., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lhvasialho M.H., Levesha M.A., Lloyd G., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConachle L.J., McElroy K., McKernan A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Pillingmore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehara H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann K.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whitlaker P., Willey D.L., Williams L., Williams S.A., Wilmington L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP FUNCTION, AND MUTAGENESIS OF GLU-87; GLU-88; CYS-124; ASP-120 AND ASP-138.
 RX PubMed=11084335;
 RA Vucic D., Stennicke H.R., Pisabarro M.T., Salvesen G.S., Dixit V.M.;
 RT "MI-IAP, a novel inhibitor of apoptosis that is preferentially expressed in human melanomas.";
 RL Curr. Biol. 10:1359-1366(2000).
 RN [7]
 RP INTERACTION WITH SMAC.
 RX PubMed=11801603;
 RA Vucic D., Deshayes K., Ackerly H., Pisabarro M.T., Kadhodayan S., Fairbrother W.J., Dixit V.M.;
 RT "SMAC negatively regulates the anti-apoptotic activity of melanoma inhibitor of apoptosis (MI-IAP)."
 RL J. Biol. Chem. 277:12275-12279(2002).
 RN [8]
 RP ACTIVATION OF MAP KINASES.
 RX PubMed=11865055;
 RA Sanna M.G., da Silva Correia J., Ducrey O., Lee J., Nomoto K., Schrantz N., Devereaux Q.L., Ulevitch R.J.;
 RT "IAP suppression of apoptosis involves distinct mechanisms: the TAK1/JNK1 signaling cascade and caspase inhibition.";
 RL Mol. Cell. Biol. 22:1754-1766(2002).
 RN [9]
 RP FUNCTION: Protects against apoptosis induced by TNF or by chemical agents such as adriamycin, etoposide or staurosporine. Suppression of apoptosis is mediated by activation of MAPK/JNK1, and possibly also of MAPK9/JNK2. This activation depends on TAB1 and NR2C2/TAK1. In vitro, inhibits caspase-3 and proteolytic activation of pro-caspase-9. Isoform 1 blocks staurosporine-induced apoptosis and isoform 2 blocks etoposide-induced apoptosis.
 CC SUBUNIT: Binds to caspase-9. Interaction with SMAC via the BIR domain disrupts binding to caspase-9 and apoptotic suppressor activity. Interacts with TAB1. In vitro, interacts with caspase-3 and caspase-7 via its BIR domain.
 CC SUBCELLULAR LOCATION: Nuclear, and in a filamentous pattern throughout the cytoplasm.
 CC ALTERNATIVE PRODUCTS: 3 isoforms, 1/Livin beta, 2/Livin alpha

Db 228 ARLETFEAMPNRNLKOKPHOLAEAGFFYGVGDRVRCFSCGGSLMDMNDDEPMQHALML 287
QY 64 PGCKYLLEEKHEXINNHLRSLLEGALVQTTKTPSLTKRISDTIFPNPML----QEAI 119
Db 288 SOCRFVKLMKGQLYI-----DTVAAPVLAEEKKEEST 319
QY 120 RMGFEDFKVKKIMEERIQTSGSNYKTLLEVAVADLVSAQKDTT--ENELNOTSLQREISPE 177
Db 320 SIGGDTYASTQASEEEOQTSLSSSEAVSGDVAPSVAPTATRIENKIYEATAVATPSTWS 379
QY 178 EPLRLQEEKLCICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKQRFVMS 236
Db 380 SGSTSIPEERKCKICGAEYNTAFLPCGHVYACAKCASSVTCKPLCRKPFDTVMRYFS 438

Search completed: June 19, 2003, 10:07:37
Job time : 25 secs


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RESULT 2
US-09-201-936-4
; Sequence 4, Application US/09201936
; Publication No. US20020187946a1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-201-936-4

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Query Match	83.2%	Score 1052;	DB 9;	Length 497;
Best Local Similarity	80.1%	Pred. No. 3.6e-92;		
Matches 189;	Conservative 25;	Mismatches 22;	InDels 0;	Gaps 0
QY	1	MTGEARLLTFGTWMSYVKNKQLARAGFYAIGEDKRVGCFHGGGLANWKPKEDPWEQHA	60	
DB	262	MADEVEARITFFGTWISYVKNKQLARAGFYALGEBGVKACFHGGGLTDMKSEDDPWEQHA	321	
QY	61	KWPGCCYLLLEEKGHETINNHLTRLEGALVOTTKTPSLTKRISDTIFPNMLQEAR	120	
DB	322	KWPGCCYLLLEOKQOEYINNHLTHLSLEECVTRTEKTPSLTRRIDPTIFONPMQEAR	381	
QY	121	MGEFDFKVKRIMEIRIOTSGSNKYTELEVADIVSAOKOTENENIOTSLQREISPEEPL	180	
DB	382	MGEFDFKVKRIMEIRIOTSGSNKYTELEVADIVSAOKOTENENIOTSLQREISPEEPL	441	
QY	181	RLRQEKRLCKICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMSCAVIDFKRIVMS	236	
DB	442	RLRQEKRLCKICMDRNIAYVVFIPCGHLVTCQCAEAVDRCPMCTVITFFKRIFMS	497	
RESULT 3				
US-09-974-592-4				
Sequence 4, Application US/09974592				
Patent No. US20020120121A1				
GENERAL INFORMATION:				
APPLICANT: Korneluk, Robert G				
APPLICANT: Mackenzie, Alexander E				
APPLICANT: Liston, Peter				
APPLICANT: Baird, Stephen				
APPLICANT: Tsang, Benjamin K				
APPLICANT: Pratt, Christine				
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND				
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE				
TITLE OF INVENTION: DISEASE				
FILE REFERENCE: 07891/009004				
CURRENT APPLICATION NUMBER: US/09/974,592				
CURRENT FILING DATE: 2001-10-09				
PRIOR APPLICATION NUMBER: US 09/617,053				
PRIOR FILING DATE: 2000-07-14				
PRIOR APPLICATION NUMBER: US 08/800,929				

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? PRIOR FILING DATE: 1997-02-13
? NUMBER OF SEQ ID NOS: 17
? SOFTWARE: FASTSEQ for Windows Version 4.0.0
? SEQ ID NO: 4
? LENGTH: 497
? TYPE: PRT
? ORGANISM: Homo sapiens
? OS-09-974-552-4

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Query Match	83.2%	Score 1052;	DB 10;	length 497;
Best Local Similarity	80.1%	Pred. No. 3.6e-92;		
Matches	189;	Conservative	25;	Mismatches 22;
			Indels	0;
			Gaps	0

[illegible]

RESULT 4

; Sequence 10, Application US/09201936
; Publication No. US20020187946A1

```

APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201, 936
EARLIER FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011, 356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576, 956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511, 485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 496
TYPE: PRT
ORGANISM: Mus musculus
IS-09-201-936-10

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Query Match	78.2%;	Score 989;	DB 9;	Length 496;
Best Local Similarity	75.8%;	Pred. No. 3.8e-86;		
Matches 179;	Conservative 27;	Mismatches 30;	Indels 0;	Gaps 0

QY	1	MTGCEALITLTCGMMYSVYNKCOLARAGAYALGOGEKVOCFHCGGGGLANMKPRKDDPEHOA	60
		: : : : :	
	261	MAEEAEAVITVFPTIITSYNKCOLARAGAYALGEGDKVKCFHCGGGGLTDMKPSDDPDHQA	320
Db		: : : : :	
QY	61	KMTPGCKYLLLEBKCHEYITNNIHLTRSDGALVQTTKTPSLTKRISDTTFPNMDLQFAIR	120
		: : : : :	
Db	321	KCTPGCKYLLLDEKOEYITNNIHLTHLPLEESLGRTEKPTPLKRIIDDTTFQNMVQBAIR	380
QY	121	MGDFDKVKKIMEERIQTSGSNYTLTLEVLAVDLVAQKDTTENELQTSLOREISPEEL	180


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Query Match      36.9%; Score 466.5; DB 10; Length 604;
Best Local Similarity 30.7%; Pred. No.4,1e-36;
Matches 110; Conservative 40; Mismatches 81; Indels 127; Gaps 8

QY      1  MTGGEARLITFGTWMYS--VKKEQIARAGFAIGEDKDVOCFHCGGLANMKPKEDPMEQ 58
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      252  MQTHAARKTEFFNPNSSVLVNPEDQASAGFYVGSNDVKFCEDCGRLCHMESGDDPWQ 311
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      59  HAKYPPGCKYILLEKGHEVINNI-----HLTRLEGALVOTTKTPSLTKRIS----- 106
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      312  HAKMFPPCEYLIRIKGOEFIRQVAVSYPHLEOL-----LSTSPSGDENASSIHLHP 366
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      107  -----DIFPN-PMLOEAINMGDFPKYVKIMEERIOTSGSNKTLVLVADVYSAKD 159
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      367  GEDHSEDAIMNNTFYVINAAYEMGFSRSLVKOTVORKILATGENTRLVNDVLIDLAHDE 426
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      160  -----TTENEIN----- 166
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      427  IREERERATERESNDLLIRKNRMALFQHLTCVPIILDSLVLVAGIINQEHYIKQT 486
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      167  QTSIQ----- 178
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      487  QTSIQARELIDTILYKGINAATVFRNSLOEAAVLYEHLFVQODIKYIPTEDVSLPVE 546
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      179  PLRLROEKLKICMDRYIAVVFIPCGHLVCKCOAEADRCPMCSAVIDEKORVFS 236
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      547  QLRLLPERIRCKVCMDEKVSIVIFPCGLLVYCKDCAPSLKRCPICRSTIKGTVTFLS 604
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 8
US-08-464-588-2
: Sequence 2, Application US/08464588
: Publication No. US20030073159A1
: GENERAL INFORMATION:
: APPLICANT: HE, ET AL.
: TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CARELLA, BYRNE, BAIN, GIUFFILIAN,
: ADDRESSEE: CECCHI, STEWART & OLSTEIN
: STREET: 6 BECKER FARM ROAD
: CITY: ROSELAND
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07068
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 INCH DISKETTE
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WORD PERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464,588
: FILING DATE: June 5, 1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/05922
: FILING DATE: 11 MAY 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: FERRARO, GREGORY D.
: REGISTRATION NUMBER: 36,134
: REFERENCE/DOCKET NUMBER: 325800-387
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-994-1700
: TELEFAX: 201-994-1744
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 438 AMINO ACIDS
: TYPE: AMINO ACID
: STRANDEDNESS:
: TOPOLOGY: LINEAR
: MOLECULE TYPE: PROTEIN
: US-08-464-588-2

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[illegible]

	RESULT 9	
	US-10-323-643-2	
	; Sequence 2, Application US/10323643	
	; Publication No. US20030108552A1	
	; GENERAL INFORMATION:	
	; APPLICANT: He, et al.	
	; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1	
	; FILE REFERENCE: PF165P1D1	
	; CURRENT APPLICATION NUMBER: US/10/323,643	
	; CURRENT FILING DATE: 2002-12-20	
	; PRIOR APPLICATION NUMBER: 08/464,568	
	; PRIOR FILING DATE: 1995-06-05	
	; PRIOR APPLICATION NUMBER: PCT/US95/05922	
	; PRIOR FILING DATE: 1995-05-11	
	; NUMBER OF SEQ ID NOS: 10	
	; SOFTWARE: PatentIn version 3.1	
	; SEQ ID NO 2	
	LENGTH: 438	
	TYPE: PRt	
	ORGANISM: Homo sapiens	
	US-10-323-643-2	
QY	Query Match	36.3%; Score 458.5; DB 9; Length 438;
Db	Best Local Similarity	29.5%; Pred.No.1.5e-35;
	Matches 104; Conservative 50; Mismatches 82; Indels 117; Gaps 6;	
QY	1 MTGEATLLFTTGTMYS--VAKBOLAAAGFAIGDEKRGVCFHGGGLAMKKPEDDPWEO 58	
Db	86 MQTHAAKRRTFMYPSSVPVQPEOLASAGEFYVRNDVVCFCDCDGLRWESGDDPWVE 145	
QY	59 HAKWPGCKYLLEKRGHEIYINNI-----HLTRLEGALVOYTKKT-----PSLTR 104	
Db	146 HAKWPCECFELIRKKGDFVDEIGRYPHLLEQLLSTDPDTGGEADNPRIHFEGPGRSSS 205	
QY	105 ISDIIFRNPMQELIRMGFDEKDVKKIMEERIQSGSNKYTLLEVLYADVLSAQDITENE 164	
Db	206 EDAYMANTPVAKSLENGFNVDIKQTVOASKILTTGENYKTVANDIVSALLNAEDKEREE 265	
QY	165 -----LNQTSIQ 171	
Db	266 KEQAEMASDDSLIRKNRMALFQOLTGVLPILDNLKANVINKEGHDIHKOTQPLQ 325	
QY	172 -RE-----ISPEEPIRLR 183	

```
D0      .    326 ARELIDTLVAGNNAANFIKNCKRIDSTLYKXNLFPDKMMKIPTEDVSLSLEEQRLRLL   385S  
QY        184 QEKLTKICIMDRYTAVVFIPCGHLVTYCQAEEADVRCPMCASVIDFKORYEMS     236  
          ||| :||::| ::||||| | | | | : : |:|-| :-|  
D0       386 QEERTCKVCMDKEYSVVFI PCGHLVQCQEAPSLRKPCIRGLIKGTVRFTLS     438
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```

RESULT 10
US-10-153-668-338
: Sequence 338, Application US/10153668
: Publication No. US20030092616A1
GENERAL INFORMATION:
APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
APPLICANT: MORAMATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STATE Activating Gene
FILE REFERENCE: 1254-0207P
CURRENT APPLICATION NUMBER: 2002-05-24
PRIORITY FILING DATE: 2002-05-24
PRIORITY APPLICATION NUMBER: US/10/153, 668
PRIORITY FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: US 60/315, 031
PRIORITY FILING DATE: 2001-08-31
PRIORITY APPLICATION NUMBER: US 60/328, 403
PRIORITY FILING DATE: 2001-10-12
PRIORITY APPLICATION NUMBER: JP 2001-157043
PRIORITY FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: JP 2001-260681
PRIORITY FILING DATE: 2001-08-30
PRIORITY APPLICATION NUMBER: JP 2001-313175
PRIORITY FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 338
LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-668-338

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Query Match          36.3%; Score 458.5; DB 9; Length 618;
  Best Local Similarity 29.5%; Pred. No. 2.5e-35;
Matches 104; Conservative 50; Mismatches 82; Indels 117; Gaps 6

QY      1 MTGPEARLITEGTWMTS--VNKEOLARGFYAIGQEDVKVOCFHCGGLANMKPKEDPMQ 58
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      266 MQTHAARTRTFMWPSSVPVQPEOLASAGEYFVVGVNDVKCPCCGGGLRCWESGDPMWE 325
      266 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      59 HAKYIPGCKYLLIEKGHEYYNNI-----HLRSLGALVQTTKT-----PSLKR 104
      59  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      326 HAKMPPREFELIRMGGEFVDEIGGRYPHLLLEQLLSTSDTGEENADPIIHFGGESSS 385
      326 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      105 ISDTFPPMLOEALRMGFDFDKYKIMBERIOTSGSNVKTLEVLVADVSOKOPLTE 164
      105 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      386 EDAYVMNTPVYKSALEMGFNRDLYKQVOSKITLTGENTKYNDIVSALLNADEREERE 445
      386 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      165 -----LNQTSIQ 171
      165 -----: : : : : : : : : : : : : : : : : : : : : : : : : :

Db      446 KEQKAEASDDLIRKNRMALFQQLTCVLPIDLNLLKANYINKQEHDIKQKQIPRLQ 505
      446 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      172 -RE-----ISPEEPLRL 183
      172 -RE-----: : : : : : : : : : : : : : : : : : : : : : : : : :
      172 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db      506 ARELIDTILVKGNAANIFKNCLKEIDSTLYKNLEFVDKKNMKYIPTEDVSGLELEQLRL 565
      506 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      184 QEERICKICMORYIAVFPQGHLYWCQACARVDCPMCSAVIDEFKOVFMS 236
      184 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      184 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db      566 QEERICKCMDESVFIPQGHLYWCQACASLRCRIGIIGVTFEIS 618
      566 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 11
US-09-974-592-12
; Sequence 12, Application US/09974592
; Patent No. US20020120121A1

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? GENERAL INFORMATION:
? APPLICANT: Korneluk, Robert G
? APPLICANT: Mackenzie, Alexander E
? APPLICANT: Liston, Peter
? APPLICANT: Baird, Stephen
? APPLICANT: Tsang, Benjamin K
? APPLICANT: Pratt, Christine
? TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
? TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
? TITLE OF INVENTION: DISRASE
? FILE REFERENCE: 07891/009004
? CURRENT APPLICATION NUMBER: US/09/974,592
? CURRENT FILING DATE: 2001-10-09
? PRIOR APPLICATION NUMBER: US 09/617,053
? PRIOR FILING DATE: 2000-07-14
? PRIOR APPLICATION NUMBER: US 08/800,929
? PRIOR FILING DATE: 1997-02-13
? NUMBER OF SEQ ID NOS: 17
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 12
? LENGTH: 600
? TYPE: PR1
? ORGANISM: Mus musculus
US-09-974-592-12

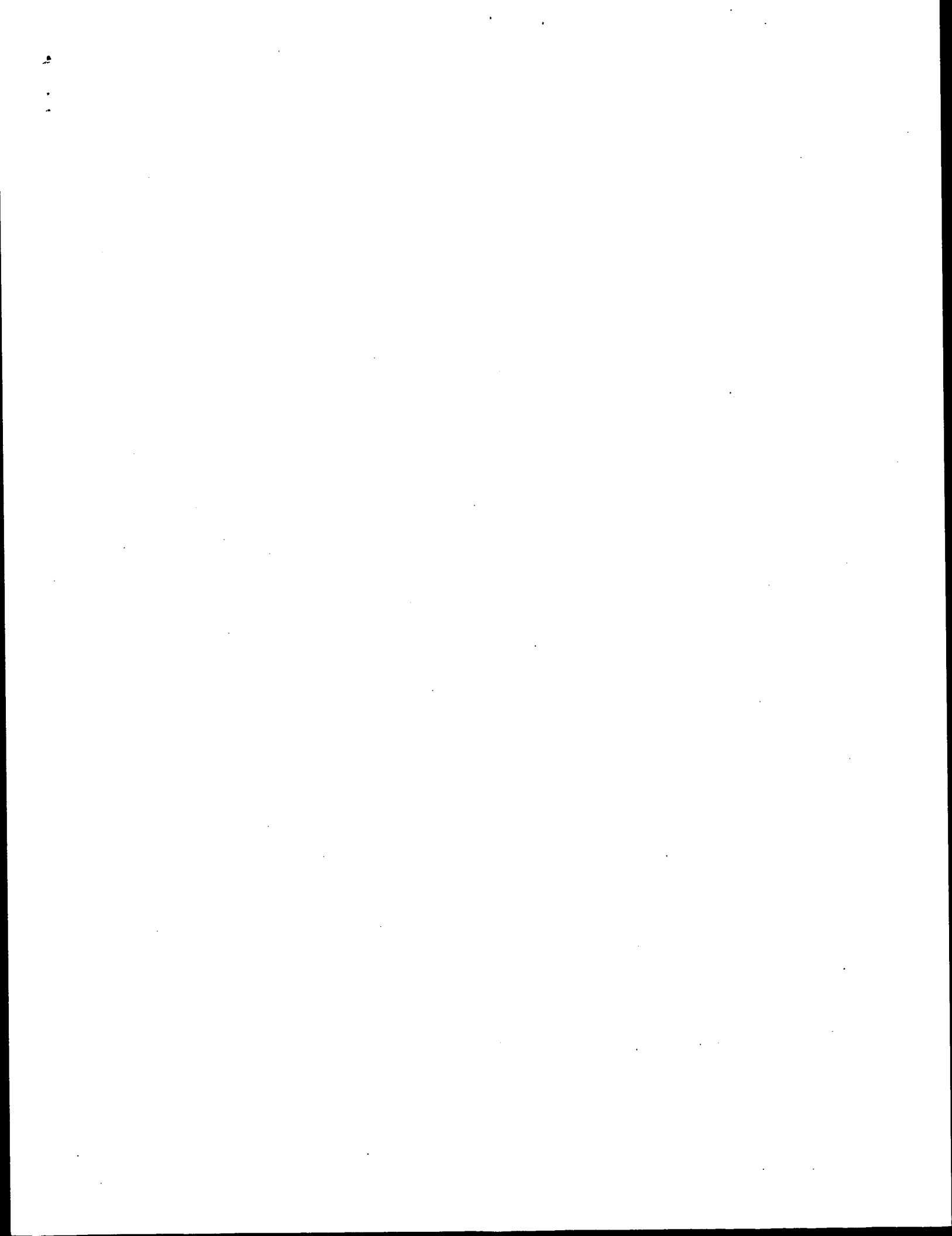
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RESULT 12
US-09-201-936-8
; Sequence 8, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneiluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Iliston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/1996/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:07:05 ; Search time 15 Seconds
(without alignments)
462,921 Million cell updates/sec

Title: US-10-024-433-2

Sequence: 1 MTGEYARLITFGTWMYSVKNK.....VDRCPMSAVIDFKQVPM 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1264	100.0	236	US-09-121-979-4	Sequence 4, Appl 1
2	1264	100.0	236	US-09-332-319-4	Sequence 4, Appl 1
3	1264	100.0	236	US-09-239-867-2	Sequence 2, Appl 1
4	1052	83.2	236	US-09-239-867-4	Sequence 4, Appl 1
5	1052	83.2	497	US-08-511-485-4	Sequence 4, Appl 1
6	1052	83.2	497	US-09-212-971-4	Sequence 4, Appl 1
7	1052	83.2	497	US-08-800-929A-4	Sequence 4, Appl 1
8	1052	83.2	497	US-09-617-053A-4	Sequence 4, Appl 1
9	989	78.2	496	US-08-511-485-10	Sequence 10, Appl 1
10	989	78.2	496	US-09-212-971-10	Sequence 10, Appl 1
11	989	78.2	496	US-08-800-929A-10	Sequence 10, Appl 1
12	989	78.2	496	US-09-617-053A-10	Sequence 10, Appl 1
13	472.5	37.4	604	US-08-569-749-4	Sequence 4, Appl 1
14	472.5	37.4	604	US-08-569-749-2	Sequence 2, Appl 1
15	466.5	36.9	604	US-08-511-485-6	Sequence 6, Appl 1
16	466.5	36.9	604	US-09-212-971-6	Sequence 6, Appl 1
17	466.5	36.9	604	US-08-800-929A-6	Sequence 6, Appl 1
18	466.5	36.9	604	US-09-617-053A-6	Sequence 6, Appl 1
19	458.5	36.3	618	US-08-569-749-2	Sequence 2, Appl 1
20	458.5	36.3	618	US-08-569-749-2	Sequence 2, Appl 1
21	458.5	36.3	618	US-09-069-023-29	Sequence 29, Appl 1
22	458.5	36.3	618	US-09-069-023-29	Sequence 29, Appl 1
23	455.5	36.0	600	US-09-212-971-12	Sequence 12, Appl 1
24	455.5	36.0	600	US-08-800-929A-12	Sequence 12, Appl 1
25	455.5	36.0	600	US-09-617-053A-12	Sequence 12, Appl 1
26	454.5	36.0	618	US-08-511-485-8	Sequence 8, Appl 1
27	454.5	36.0	618	US-09-212-971-8	Sequence 8, Appl 1

28	454.5	36.0	618	US-08-800-929A-8	Sequence 8, Appl 1
29	454.5	36.0	618	US-09-617-053A-8	Sequence 8, Appl 1
30	443	35.0	612	US-09-212-971-14	Sequence 14, Appl 1
31	443	35.0	612	US-08-800-929A-14	Sequence 14, Appl 1
32	443	35.0	612	US-08-569-749-14	Sequence 14, Appl 1
33	443	35.0	612	US-09-617-053A-14	Sequence 14, Appl 1
34	443	35.0	612	US-09-617-053A-14	Sequence 14, Appl 1
35	440	31.6	498	US-08-511-485-13	Sequence 13, Appl 1
36	347	27.5	66	US-08-511-485-25	Sequence 25, Appl 1
37	334	26.4	66	US-08-511-485-12	Sequence 24, Appl 1
38	314.5	24.9	275	US-08-836-134-21	Sequence 12, Appl 1
39	314.5	24.9	275	US-08-836-134-21	Sequence 21, Appl 1
40	314.5	24.9	275	US-09-493-784-21	Sequence 21, Appl 1
41	312.5	24.7	268	US-08-836-134-22	Sequence 22, Appl 1
42	312.5	24.7	268	US-09-493-784-22	Sequence 22, Appl 1
43	262	20.7	50	US-08-975-080-28	Sequence 28, Appl 1
44	262	20.7	50	US-08-975-080-29	Sequence 29, Appl 1
45	262	20.7	50	US-08-975-080-32	Sequence 32, Appl 1

ALIGNMENTS

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RESULT 1
US-09-121-979-4
; Sequence 4, Application US/09121979
; Patent No. 6159709
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021001
; CURRENT APPLICATION NUMBER: US/09/121,979
; CURRENT FILING DATE: 1998-07-24
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-979-4

Query Match      100.0%; Score 1264; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.6e-127;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTGEYARLITFGTWMYSVKNKQARAGFYAIGQEDKVCFCGGLANWKPKEDPWEQHA 60
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DB      1 MTGEYARLITFGTWMYSVKNKQARAGFYAIGQEDKVCFCGGLANWKPKEDPWEQHA 60

QY      61 KMYGCKYLLKKEGHEYYNNHILTRSLGALVOTTKTPSLTKRISDTIFPPMLQEAIR 120
      |||||||
DB      61 KMYGCKYLLKKEGHEYYNNHILTRSLGALVOTTKTPSLTKRISDTIFPPMLQEAIR 120

QY      121 MGFDKVKYKIMERIOTSGSNKYTLLEVADVADVSAQDTEENELQTSLOREISPEEPL 180
      |||||||
DB      121 MGFDKVKYKIMERIOTSGSNKYTLLEVADVADVSAQDTEENELQTSLOREISPEEPL 180

QY      181 RRLQEKIKCTCMQRIYAVITPCGHLYTCQCAAVVDRCPMSAVIDFKQVPM 236
      |||||||
DB      181 RRLQEKIKCTCMQRIYAVITPCGHLYTCQCAAVVDRCPMSAVIDFKQVPM 236

RESULT 2
US-09-332-319-4
; Sequence 4, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF

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FILE REFERENCE: 07891/021002
CURRENT APPLICATION NUMBER: US/09/332,319
CURRENT FILING DATE: 1999-06-14
EARLIER APPLICATION NUMBER: 09/121,979
EARLIER FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 236
TYPE: PRF
ORGANISM: Homo sapiens
US-09-332-319-4

Query Match 100.0%; Score 1264; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.6e-127;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGYEARLITFGTWMYSVKNKQOLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
DB 1 MTGYEARLITFGTWMYSVKNKQOLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
QY 61 KWPYCKYLLKKEGHEYNINHLTRSLGALVQTTKTPSLTKRISDTIFPMPMOEAIR 120
DB 61 KWPYCKYLLKKEGHEYNINHLTRSLGALVQTTKTPSLTKRISDTIFPMPMOEAIR 120
QY 121 MGDFDKVKKIMEERIQSGSNKYLEVLVADLVSAQKDTENELNQSLOREISPEEPL 180
DB 121 MGDFDKVKKIMEERIQSGSNKYLEVLVADLVSAQKDTENELNQSLOREISPEEPL 180
QY 181 RRLQEKIKICKMDRITAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKORVEMS 236
DB 181 RRLQEKIKICKMDRITAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKORVEMS 236

RESULT 3
US-09-239-867-2

Sequence 2, Application US/09239867
Patent No. 6331412
GENERAL INFORMATION:
APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/09/239,867
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 236
TYPE: PRF
ORGANISM: Homo sapiens
US-09-239-867-2

Query Match 100.0%; Score 1264; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.6e-127;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 KWPYCKYLLKKEGHEYNINHLTRSLGALVQTTKTPSLTKRISDTIFPMPMOEAIR 120
QY 121 MGDFDKVKKIMEERIQSGSNKYLEVLVADLVSAQKDTENELNQSLOREISPEEPL 180
DB 121 MGDFDKVKKIMEERIQSGSNKYLEVLVADLVSAQKDTENELNQSLOREISPEEPL 180
QY 181 RRLQEKIKICKMDRITAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKORVEMS 236
DB 181 RRLQEKIKICKMDRITAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKORVEMS 236

DB 181 RRLQEKIKICKMDRITAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKORVEMS 236

RESULT 4
US-09-239-867-4

Sequence 4, Application US/09239867
Patent No. 6331412
GENERAL INFORMATION:
APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/09/239,867
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 236
TYPE: PRF
ORGANISM: Homo sapiens
US-09-239-867-4

Query Match 83.2%; Score 1052; DB 4; Length 236;
Best Local Similarity 80.1%; Pred. No. 1.3e-104;
Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

QY 1 MTGYEARLITFGTWMYSVKNKQOLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
DB 1 MADEEARLITFGTWMYSVKNKQOLARAGFYAIGQEDKVCFCGCGGLTDMKPSDPEQHA 60
QY 61 KWPYCKYLLKKEGHEYNINHLTRSLGALVQTTKTPSLTKRISDTIFPMPMOEAIR 120
DB 61 KWPYCKYLLKKEGHEYNINHLTRSLGALVQTTKTPSLTKRISDTIFPMPMOEAIR 120
QY 121 MGDFDKVKKIMEERIQSGSNKYLEVLVADLVSAQKDTENELNQSLOREISPEEPL 180
DB 121 MGDFDKVKKIMEERIQSGSNKYLEVLVADLVSAQKDTENELNQSLOREISPEEPL 180
QY 181 RRLQEKIKICKMDRITAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKORVEMS 236
DB 181 RRLQEKIKICKMDRITAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKORVEMS 236

RESULT 5
US-08-511-485-4

Sequence 4, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 07540/002001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 497 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: both
 MOLECULE TYPE: protein
 US-08-511-485-4

Query Match 83.2%; Score 1052; DB 2; Length 497;
 Best Local Similarity 80.1%; Pred. No. 4e-104;
 Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

QY 1 MTGTEARLITFTGWTMSYKNEQLARAGFYALGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
 DB 262 MADYEARIFFGTWITSYKNEQLARAGFYALGEGDKVCFCGCGGLTDMKPSDEPWEQHA 321
 QY 61 KWPYGCYLLKEKGHEYYNNHILTRSLGALVOTTKTPSLTKISDTFFPNMLOEAR 120
 DB 322 KWPYGCYLLKEKGHEYYNNHILTRSLGALVOTTKTPSLTKISDTFFPNMLOEAR 381
 QY 121 MGDFDKVKIMEIRIOTSGSNYKTELEVADLVSAQKDTTENELNQTSLQREISPEPL 180
 DB 382 MGDFDKVKIMEIRIOTSGSNYKTELEVADLVSAQKDTTENELNQTSLQREISPEPL 441
 QY 181 RLQOEKLCIKCMRNIAYVFPCHLVTCKQCAEAVDRCPMCAVIDPKQVENS 236
 DB 442 RLQOEKLCIKCMRNIAYVFPCHLVTCKQCAEAVDRCPMCAVIDPKQVENS 497

RESULT 6
 US-09-212-971-4
 Sequence 4, Application US/09212971B
 Patent No. 6107041
 GENERAL INFORMATION:
 APPLICANT: Korneluk, Robert G
 APPLICANT: Mackenzie, Alexander E
 APPLICANT: Liston, Peter
 APPLICANT: Baird, Stephen
 APPLICANT: Tsang, Benjamin K
 TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
 TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
 TITLE OF INVENTION: DISEASE
 FILE REFERENCE: 07891/009002
 CURRENT APPLICATION NUMBER: US/09/212,971B
 CURRENT FILING DATE: 1998-12-16
 EARLIER APPLICATION NUMBER: 60/017,354
 EARLIER FILING DATE: 1996-04-26
 EARLIER APPLICATION NUMBER: 60/030,590
 EARLIER FILING DATE: 1996-11-14
 EARLIER APPLICATION NUMBER: 08/800,929
 EARLIER FILING DATE: 1997-02-13
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 497
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-212-971-4

Query Match 83.2%; Score 1052; DB 3; Length 497;
 Best Local Similarity 80.1%; Pred. No. 4e-104;
 Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;
 1 MTGTEARLITFTGWTMSYKNEQLARAGFYALGQEDKVCFCGCGGLANMKPKEDPWEQHA 60

DB 262 MADYEARIFFGTWITSYKNEQLARAGFYALGEGDKVCFCGCGGLTDMKPSDEPWEQHA 321
 QY 61 KWPYGCYLLKEKGHEYYNNHILTRSLGALVOTTKTPSLTKISDTFFPNMLOEAR 120
 DB 322 KWPYGCYLLKEKGHEYYNNHILTRSLGALVOTTKTPSLTKISDTFFPNMLOEAR 381
 QY 121 MGDFDKVKIMEIRIOTSGSNYKTELEVADLVSAQKDTTENELNQTSLQREISPEPL 180
 DB 382 MGDFDKVKIMEIRIOTSGSNYKTELEVADLVSAQKDTTENELNQTSLQREISPEPL 441
 QY 181 RLQOEKLCIKCMRNIAYVFPCHLVTCKQCAEAVDRCPMCAVIDPKQVENS 236
 DB 442 RLQOEKLCIKCMRNIAYVFPCHLVTCKQCAEAVDRCPMCAVIDPKQVENS 497

RESULT 7
 US-08-800-929A-4
 Sequence 4, Application US/08800929A
 Patent No. 6133437
 GENERAL INFORMATION:
 APPLICANT: Korneluk, Robert G
 APPLICANT: Mackenzie, Alexander E
 APPLICANT: Liston, Peter
 APPLICANT: Baird, Stephen
 APPLICANT: Tsang, Benjamin K
 TITLE OF INVENTION: DETECTION AND MODULATION OF
 TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
 TITLE OF INVENTION: DISEASE
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Clark & Elbing LLP
 STREET: 176 Federal Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/800,929A
 FILING DATE: 13-FEB-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/030,590
 FILING DATE: 14-NOV-1996
 APPLICATION NUMBER: 60/017,354
 FILING DATE: 26-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Bleker-Brady, Kristina
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 07891/009001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-428-0200
 TELEFAX: 617-428-7045
 TELEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 497 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-800-929A-4

Query Match 83.2%; Score 1052; DB 4; Length 497;
 Best Local Similarity 80.1%; Pred. No. 4e-104;
 Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

Db 321 KCVPGKYLDEKGOEYINNIHLPLLESIGRTAEKPEPLTKKIDDTIFQPMQOEAR 380
QY 121 MGDFKRYKIMERIOTSGSNYKTELEVADLVSAQKOTENELNOSTLOREISPEEL 180
Db 381 MGSFKLKTMEKRIOTSGSSYSLLEVLIADLVSAQKDNTEDESSQTSLOKDISTEEQL 440
QY 181 RRLQERKCKICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMCAVIDEKOQVEMS 236
Db 441 RRLQERKCKICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMCAVIDEKOQVEMS 496

RESULT 13

US-08-569-749-4
; Sequence 4, Application US/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rotne, Mike
; APPLICANT: Goeddel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,749
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 604 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-569-749-4

Query Match 37.4%; Score 472.5; DB 4; Length 604;
Best Local Similarity 31.0%; Pred. No. 5.9e-42;
Matches 111; Conservative 40; Mismatches 80; Indels 127; Gaps 8;

QY 1 MTGEARLITFGTWYS--VNKEOLARAGFYAIGQEDKYOCFHCGGLANMKPKEDPMQ 58
Db 252 MGTAAARKTFFNPPSSVLPNEQLASAGFYVGSDDVKCFCCDGLRWESGDDPMQ 311
QY 59 HAKVPGCKYLLEEGHEHYNNI-----HLTSLGALVQTKTKPSLTKRIS----- 106
Db 312 HAKVPPREYLLIRIGQEFIRQVQASYPHLEQL-----LSTSDSPGDENASSIHFEP 366
QY 107 -----DITFNP-PMLOAIIMGDFPKDYKIMERIOTSGSNYKTELEVADLVSAQK 159
Db 367 GEDHSDAIAIMNTFVINAAVEMGFSRLVKQTVQKRIATGENYRLVNDLVLDLNAEDE 426
QY 160 -----TTENELN----- 166
Db 427 IREERERATPEKESNDLLLRKNMALFQHLTCVPIILDSLLTAGIINEQEHVYKOT 486

QY 167 QTSLO-----REISPEE 178
Db 487 QTSLOARELIDTILVGNIAATVFRNSLOAEAVLEHLWQODIKYIPEDEVADLPVEE 546
QY 179 PLRLQERKCKICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMCAVIDEKOQVEMS 236
Db 547 QLRLOERKCKICMDREYSIVIFPCGHLVVCADAPSLRCPICRSTIGTGYVTFELS 604

RESULT 14

PCT-US96-12860-4
; Sequence 4, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 604 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-12860-4

Query Match 37.4%; Score 472.5; DB 5; Length 604;
Best Local Similarity 31.0%; Pred. No. 5.9e-42;
Matches 111; Conservative 40; Mismatches 80; Indels 127; Gaps 8;

QY 1 MTGEARLITFGTWYS--VNKEOLARAGFYAIGQEDKYOCFHCGGLANMKPKEDPMQ 58
Db 252 MGTAAARKTFFNPPSSVLPNEQLASAGFYVGSDDVKCFCCDGLRWESGDDPMQ 311
QY 59 HAKVPGCKYLLEEGHEHYNNI-----HLTSLGALVQTKTKPSLTKRIS----- 106
Db 312 HAKVPPREYLLIRIGQEFIRQVQASYPHLEQL-----LSTSDSPGDENASSIHFEP 366
QY 107 -----DITFNP-PMLOAIIMGDFPKDYKIMERIOTSGSNYKTELEVADLVSAQK 159
Db 367 GEDHSDAIAIMNTFVINAAVEMGFSRLVKQTVQKRIATGENYRLVNDLVLDLNAEDE 426
QY 160 -----TTENELN----- 166
Db 427 IREERERATPEKESNDLLLRKNMALFQHLTCVPIILDSLLTAGIINEQEHVYKOT 486
QY 167 QTSLO-----REISPEE 178

Db 487 QTSQARLRIDITILYKGNIAATVFNSLSQEAALVLEHLEFVQODITYIPTEDVSDLPVEE 546

Oy 179 PLRLROEKLCKICMDRYIAVYFIPCGHLVTFCKCAEAADRCMCAVAIDFKRVFMS 236
||||| :||| : :||| || || :||| : | -|||
547 QLRRLQERTCKVCMDEVSIVFIPCGHLVTFCKCAAPSLRKCPICSTIKGVRTFLS 604

RESULT 15
US-08-511-485-6
; Sequence 6, Application US/08511485

; GENERAL INFORMATION:

Query Match	36.9%	Score 466.5	DB 2	Length 604
Best Local Similarity	30.7%	Pred. No. 2.6e-41		
Matches 110	Conservative 40	Mismatches 81	Indels 127	Gaps 8

D_b 487 QTSIQARLEIDITILYKGNIAAVFERNLSQEAALVYLHELFVQODIKYITTEDVSDDLPVE 546

Q_y 179 PLRRLOEQEKLCKICMDRYIAVFIPCGHLVTGKCCEANDRCPMCSAVIDFKQRYFMS 236
||||| : ||||| : ::||| | | | | : ||| : - ||-|
547 QLRRLPPEERTCKVCMDKEYSIVFPCGHVLVCKDCAPSLAKCPICISFTIKGVTRFLS 604

```
Search completed: June 19, 2003, 10:09:51
Job time : 17 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:07:05 ; Search time 35 seconds
(without alignments)
898.490 Million cell updates/sec

Title: US-10-024-433-2
Perfect score: 1264

Sequence: 1 MTEGARLITFGTMTSVNK.....VDRCPMCSAVIDFKRVFMS 236

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq_101002:*
2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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9: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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19: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
20: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1264	100.0	236	21	Human TIAP (an inh
2	1264	100.0	236	23	Human testes spec
3	1259	99.6	236	22	Human IAP-like pro
4	1259	99.6	236	22	Human IAP-like pro
5	1241	98.2	236	22	Human IAP-like pro
6	1237	97.9	236	22	Human IAP-like pro
7	1052	83.2	278	23	Human IAP-like pro
8	1052	83.2	497	18	Human apoptosis in
9	1052	83.2	497	19	Human XIAP protein
10	1052	83.2	497	21	Human X-linked inh

11	1052	83.2	497	23	ABG65663
12	1049	83.0	497	21	AAV59451
13	1028	81.3	496	18	AAV19745
14	989	78.2	496	18	AAV19584
15	989	78.2	496	18	AAV19584
16	989	78.2	496	18	AAV19584
17	472.5	37.4	604	18	AAV19747
18	472.5	37.4	604	18	AAV19747
19	472.5	37.4	604	20	AAV52703
20	472.5	37.4	604	20	AAV33997
21	466.5	36.9	604	18	AAV19582
22	466.5	36.9	604	19	AAV69295
23	466.5	36.9	604	23	ABG65664
24	459	36.3	116	22	AAE00364
25	458.5	36.3	438	17	AAW04583
26	458.5	36.3	618	18	AAV19746
27	458.5	36.3	618	18	AAV13545
28	458.5	36.3	618	20	AAV33998
29	455.5	36.0	600	19	AAV69298
30	454.5	36.0	618	18	AAV19583
31	454.5	36.0	618	19	AAV69296
32	454.5	36.0	618	23	ABG65665
33	443	35.0	116	22	AAE00361
34	443	35.0	612	18	AAV13555
35	443	35.0	612	19	AAV69299
36	440	34.8	116	22	AAE00363
37	440	34.8	116	22	AAE00369
38	438	34.7	116	22	AAE00360
39	437	34.6	591	18	AAV19586
40	437	34.6	591	18	ABG65668
41	436.5	34.5	115	22	AAE00362
42	435	34.4	116	22	AAE00359
43	433.5	34.3	602	23	ABG65667
44	429.5	34.0	602	18	AAV19585
45	404	32.0	498	18	AAV19748

ALIGNMENTS

RESULT 1	AAV81440	standard; Protein; 236 AA.
ID	AAV81440	
AC	AAV81440	
XX	03-JUL-2000	(first entry)
DE	Human TIAP (an inhibitor of apoptosis).	
XX	TIAP; inhibitor of apoptosis protein; IAP; X-linked IAP; XIAP.	
KW	internal ribosome entry site; IRES; human; cap-independent translation;	
KW	drug screening; cancer; autoimmune disease; degenerative disease;	
KW	immunorejection; gene therapy.	
OS	Homo sapiens.	
XX	MO200005366-A2.	
XX	03-FEB-2000.	
PD	22-JUL-1999;	99WO-IB01415.
PF	24-JUL-1998;	98US-0121979.
PR	14-JUN-1999;	99US-0332319.
XX	(UYOT-) UNIV OTTAWA.	
PA	Kornejuk RG, Holcik M, Liston P;	
PI	WPI; 2000-338644/29.	
XX	N-PSDB; AAA06940.	
DR		
XX		

Human inhibitor of
Human XIAP protein
Mouse inhibitor of
Mouse apoptosis in
Murine XIAP protei
Mouse inhibitor of
Human c-IAP2. Hom
Human cellular inh
Human apoptosis in
Human H1AP-1 prote
Human inhibitor of
Rhesus IAP-like pr
Human inhibitor of
Human c-IAP1. Hom
Human cellular inh
Murine H1AP-1 prote
Human apoptosis in
Human H1AP-2 prote
Human inhibitor of
Chimpanzee IAP-lik
Murine c-IAP. Mus
Murine H1AP-2 prote
Gorilla IAP-like p
Baboon IAP-like pr
Baboon apoptosis in
Mouse inhibitor of
Cynomolgus IAP-lik
Human IAP-like pro
Mouse inhibitor of
Mouse apoptosis in
Drosophila inhibi

PT New isolated X-linked inhibitor of apoptosis internal ribosome entry
PT site, used to develop agents for treating, e.g. cancer -
PS Disclosure; Page 82; 87pp; English.

CC The invention relates to the identification of modulators of cap-
CC independent translation and apoptosis. The method comprises exposing a
CC test compound to an X-linked inhibitor of apoptosis protein (XIAP)
CC internal ribosome entry site (IRES) reporter cistron, and determining
CC the amount of translation from the XIAP IRES reporter cistron exposed to
CC the compound relative to the translation from the unexposed XIAP IRES
CC reporter cistron. A relative increase in translation from the exposed
CC XIAP IRES reporter cistron indicates a compound that increases XIAP
CC IRES-dependent (cap independent) translation. XIAP protein plays a
CC critical role in the regulation of apoptosis by suppressing activation
CC of downstream caspase-3 and caspase-7. Compounds identified by the
CC method which decrease XIAP IRES-dependent translation (thus leading to
CC reduced expression of XIAP and hence increasing apoptosis) can be used
CC for treating cancer. The methods can also be used for the identification
CC of agents that upregulate XIAP translation and hence inhibit apoptosis,
CC which can be used to treat autoimmune diseases, degenerative diseases or
CC immunorejection. Such agents may, for example, be used to inhibit
CC apoptosis of neurons in conditions such as Alzheimer's disease, islet
CC cells in autoimmune diabetes mellitus, photoreceptor cells in retinitis
CC pigmentosa and diabetic retinopathy; and cardiomyocytes after myocardial
CC infarction. They can also be used to enhance the survival of cell or
CC organ transplants. XIAP IRES elements can also be incorporated into
CC expression constructs which encode XIAP or other IAPs (inhibitor of
CC apoptosis proteins, e.g., TIAP: AAY81440). Such constructs may be used
CC in gene therapy to inhibit apoptosis in a cell. The present sequence
CC represents human TIAP (an inhibitor of apoptosis protein), DNA encoding
CC which may be used in an expression vector comprising a XIAP IRES
CC element.

XX Sequence 236 AA;

SQ
Query Match 100.0%; Score 1264; DB 23; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.1e-119;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGFEARLITFGTWMYSVKNKQDLARAGFYAIGQEDKVCFCGCGGLANMKPREDPWEQHA 60
DB 1 MTGFEARLITFGTWMYSVKNKQDLARAGFYAIGQEDKVCFCGCGGLANMKPREDPWEQHA 60
QY 61 KWPFGCKYLLEKGGHEYYNNHILTRSLGALVQTTKTPSLTKRISDTIFPPMLOEAIR 120
DB 61 KWPFGCKYLLEKGGHEYYNNHILTRSLGALVQTTKTPSLTKRISDTIFPPMLOEAIR 120
QY 121 MGFEKDYKIMKEERIGTSGSNKYKTLVADLVSAOKDTTENELNOSTLOREISPEPL 180
DB 121 MGFEKDYKIMKEERIGTSGSNKYKTLVADLVSAOKDTTENELNOSTLOREISPEPL 180
QY 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKQVFM 236
DB 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKQVFM 236

RESULT 2

AAU75066 standard; Protein; 236 AA.

AAU75066;

23-APR-2002 (first entry)

Human testes specific inhibitor of apoptosis (TIAP) protein.

TIAP: apoptosis; testes specific inhibitor of apoptosis;
human; apoptotic; cytosolic; anti-fertility; contraceptive;
chromosome 12q22-23; transgenic animal; antibody; immunogen;
testicular cell; testicular cancer; cancer; male infertility;
male birth control; XIAP.

OS Homo sapiens.
XX US6331412-B1.
XX 18-DEC-2001.
XX 29-JAN-1999; 99US-0239867.
XX 29-JAN-1998; 98US-073001P.
XX (UYOT-) UNTV OTTAWA.
XX Korneluk RG, Lagace M;
XX WPI: 2002-105275/14.
XX N-PSDB: ABR13197.
XX
XX Nucleic acids encoding a testis specific apoptosis inhibitor protein
XX (TIAP) useful for treating testicular cancers, cancers in
XX non-testicular tissues, male infertility, and for achieving male birth
XX control -
XX
XX Example 4; Fig 4B; 29pp; English.

CC This invention relates to a novel isolated nucleic acid molecule
CC encoding a TIAP polypeptide (testes-specific inhibitor of apoptosis)
CC protein. This gene is a homologue of the X-linked XIAP gene and is
CC located on chromosome 12q22-23. The nucleotide and protein sequences of
CC the invention and vectors containing these sequences may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate TIAP expression. Additionally, the nucleotide sequence may
CC be used to express the TIAP protein by recombinant methods. Conversely,
CC antisense nucleic acid molecules may be administered to down-regulate
CC TIAP expression. The nucleotide sequence may also be used to design DNA
CC probes for diagnostic assays (e.g. polymerase chain reactions (PCR)) to
CC detect and quantitate the presence of similar nucleic acid sequences in
CC samples, to identify patients who may be in need of restorative therapy.
CC Through the production of transgenic animals and cells, the sequences
CC may also be used to study the expression and function of TIAP proteins
CC and their role in metabolism. The TIAP polypeptides may be used to
CC produce antibodies against TIAP and may be used to identify modulators
CC (agonists and antagonists) of TIAP expression and activity. An anti-TIAP
CC antibody or antagonist may also be used to down-regulate TIAP expression
CC and activity. The reagents may be used in this way for the treatment of
CC excessive or insufficient apoptosis, particularly in testicular cells.
CC In particular they are useful in diagnosing and treating testicular
CC cancers, cancers in non-testicular tissues, male infertility, and for
CC achieving male birth control. The present sequence represents the
CC human TIAP protein sequence of the invention.

XX Sequence 236 AA;

SQ
Query Match 100.0%; Score 1264; DB 23; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.1e-119;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGFEARLITFGTWMYSVKNKQDLARAGFYAIGQEDKVCFCGCGGLANMKPREDPWEQHA 60
DB 1 MTGFEARLITFGTWMYSVKNKQDLARAGFYAIGQEDKVCFCGCGGLANMKPREDPWEQHA 60
QY 61 KWPFGCKYLLEKGGHEYYNNHILTRSLGALVQTTKTPSLTKRISDTIFPPMLOEAIR 120
DB 61 KWPFGCKYLLEKGGHEYYNNHILTRSLGALVQTTKTPSLTKRISDTIFPPMLOEAIR 120
QY 121 MGFEKDYKIMKEERIGTSGSNKYKTLVADLVSAOKDTTENELNOSTLOREISPEPL 180
DB 121 MGFEKDYKIMKEERIGTSGSNKYKTLVADLVSAOKDTTENELNOSTLOREISPEPL 180
QY 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKQVFM 236
DB 181 RRLQEEKLCKICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMCSAVIDFKQVFM 236

XX	RESULT 3
XX	ID AAE00365
XX	AAE00365 standard; Protein, 236 AA.
XX	AC AAE00365;
XX	DT 19-JUN-2001 (first entry)
DE	Human IAP-like protein-2 (ILP-2) with TGFbeta modulating activity.
XX	
XX	Human, inhibitor of apoptosis; IAP-like protein-2; ILP-2;
KW	Chromosome 19q13.3-q13.4; transforming growth factor beta receptor;
KW	TGFbetaR; c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;
KW	cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;
KM	T-cell acute lymphoblastic leukaemia; neurodegenerative disease;
KM	retinal degeneration; hyperferritinlaemia-cataract syndrome; cancer;
KM	autoimmune disease; diabetes; multiple sclerosis; cystostatic.
OS	Homo sapiens.
XX	
FT	Key Location/Qualifiers
FT	Domain 7..70
FT	/label= BIR_domain
FT	/note= "Baculovirus iap repeat"
FT	188..223
FT	/label= RING_finger_domain
XX	
PN	WO200123568-A2.
XX	
PD	05-APR-2001.
XX	
PF	29-SEP-2000; 2000WO-US26735.
XX	
PR	30-SEP-1999; 99US-0157169.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
PI	Duckett C, Mlr SS;
DR	WPI: 2001-258135/26.
DR	N-PSDB; AAD03581.
XX	
PT	Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
PT	transforming growth factor beta receptor modulating activity, and the
PT	nucleic acids that encode them, useful for treating, e.g. diabetes and
PT	multiple sclerosis -
XX	
PS	Claim 1; Fig 2; 108pp; English.
XX	
CC	The present sequence is human inhibitor of apoptosis (IAP)-like protein-2
CC	(ILP-2). The hlp-2 gene is located on chromosome 19q13.3-q13.4
CC	ILP-2 comprises a single amino-terminal domain known as baculovirus iap
CC	repeat (BIR), followed by a spacer region and a carboxy-terminal ring
CC	finger domain. It interacts with transforming growth factor beta
CC	receptor (TGFbetaR) and modulates TGFbetaR activity. It also potentially
CC	inhibits apoptosis induced by overexpression of Bax or by Caspase-9 and
CC	Apf-1. It also activates c-Jun N-terminal kinase (JNK) activity. ILP-2
CC	is used in the area of genetic testing for predisposition to diseases,
CC	such as cone-rod retinal dystrophy-2, retinitis pigmentosa,
CC	glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer
CC	and hyperferritinlaemia-cataract syndrome owing to an ILP-2 deletion or
CC	mutation. The ilp is also used in the treatment of diseases associated
CC	with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,
CC	diabetes and multiple sclerosis and neurodegenerative diseases including
CC	retinal degeneration. The ILP-2 gene is also used in gene therapy for
CC	treating patients suffering from ILP-2 gene deletions or mutations.
XX	
SQ	Sequence 236 AA;
XX	
Query Match	99.6%; Score 1259; DB 22; Length 236;
Best Local Similarity	99.6%; Pred No. 3.5e-119;
Matches 235, Conservative	1; Mismatches 0; Indels 0; Gaps 0

QY		1	MFGYEARLLTFTGTMWTSYNKEQLARAGFYAIGGEDKYQCCHCGGLANWKREKDEPWECHA	60
Dd		1	MFGYEARRLLTFGTMTWSYNKEQLARAGFYAIGGEDKYQCCHCGGLANWKREKDEPWECHO	60
QY		61	KMYPGCKYLLEEGHGHIYINNHLFTRSLDEGALVOTTKTPSLTKRISDPIFPNPMLOEAIR	12
Dd		61	KMYPGCKYLLEEKGHIEYINNHLFTRSLDEGALVOTTKTPSLTKRISDPIFPNPMLOEAIR	12
QY		121	MGFDPRDYAKIMEERLQTSGSNKTELEVADLVASAOKDPTENELNQTSLOREISPEEPPL	18
Dd		121	MGFDPRDYAKIMEERLQTSGSNKTELEVADLVASAKDPTENELNQTSLOREISPEEPPL	18
QY		161	RRLQBEKCLKICMDRIAYVFIFPCGLHYTCQCAEAVDRCPMCSAVIDFKORFVMS	236
Dd		161	RRLQBEKCLKICKMDRHIAVVEIFPCGLHYTCQCAEAVDRCPMCSAVIDFKORFVMS	236
RESULT 4				
AAU75747	ID	AAU75747	standard; Protein; 466 AA.	
XX	AC	AAU75747;		
XX	DT	08-MAY-2002	(first entry)	
DE	XX	Human Inhibitor of apoptosis protein 7 (IAPL7) protein.		
XX	XX	Human; inhibitor of apoptosis 7; IAPL7; cytosolic;		
KW	XX	antiapoptotic; IAP; apoptosis; V-Rel; cancer; NF-kappaB;		
KM	XX	chromosome 19; vaccine; gene therapy; hyperproliferative disease;		
KW	XX	transgenic animal; antibody.		
OS	XX	Homo sapiens.		
FH	Key	Location/Qualifiers		
FT	Region	1..133		
FT		/note= "This sequence is specifically claimed		
FT		in claim 1 of the specification and is encoded		
PN		by the nucleic acid represented in ABK14678"		
XX		WO200210381-A1.		
PD		07-FEB-2002.		
XX		18-JUL-2001; 2001WO-EP08287.		
Pf		28-JUL-2000; 2000EP-0116452.		
PA		(MERCK) MERCK PATENT GMBH.		
PI		Hentsch B;		
DR		WPI: 2002-188741/24.		
XX		P-PsDB; ABK14677.		
PT		New inhibitor of apoptosis proteins and polynucleotides useful in		
XX		vaccines for inducing an immune response against hyperproliferative		
XX		diseases e.g. cancer		
PS		Claim 1; Page 35-36; 41pp; English.		
CC		This invention relates to the nucleic acid and protein sequences of a		
CC		novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences		
CC		have homology to the IAP (inhibitors of apoptosis) gene family which		
CC		are thought to inhibit proteins by regulating the anti-apoptotic		
CC		activity of the V-Rel and NF-kappaB family of transcription factors.		
CC		The gene for IAPL7 is located on human chromosome 19. The nucleic acids		
CC		of the invention are useful for screening to identify compounds that		
CC		stimulate or inhibit the function or level of IAPL7, where the		
CC		identified compounds are useful for treating hyper-proliferative		
CC		diseases such as cancer. The protein sequences may also be used to		
CC		identify membrane bound or soluble receptors of IAPL7 by standard		
CC		receptor binding techniques. Nucleic acids encoding IAPL7, may be used		

CC as hybridisation probes for cDNA and genomic DNA, or as primers for
 CC nucleic acid amplification reaction and the primers and probes may also
 CC be used to isolate full-length cDNAs and genomic clones encoding IAP17.
 CC The nucleic acid sequences are useful as diagnostic reagents for
 CC diagnosing a disease or a susceptibility to a disease by detecting
 CC mutations in the associated gene. The nucleic acid sequence is useful
 CC for chromosome localisation and tissue expression studies and is also
 CC useful for producing transgenic animals. The IAP17 protein sequence may
 CC also be used to generate an anti-IAP17 antibody which is useful in
 CC screening methods for detecting the effect of added compounds on the
 CC production of mRNA and protein in cells. The sequences of the invention
 CC are also useful as vaccines for inducing an immunological response in a
 CC mammal. The present sequence represents the human inhibitor of apoptosis
 CC 7 (IAP7) protein of the invention.

XX Sequence 464 AA:

Query Match 99.6%; Score 1259; DB 23; Length 464;

Best Local Similarity 99.6%; Pred. No. 9e-119;

Matches 235; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGEARLITFGTWMYVSNKEQLARAGFYAIGDEKVCFCGCGGLANMKPKEDPWEQHA 60

DB 229 MTGEARLITFGTWMYVSNKEQLARAGFYAIGDEKVCFCGCGGLANMKPKEDPWEQHA 288

QY 61 KWPFGCKYLLBEKGHEYNINHLTRSLGALVQTKTKPSLTKRISDTIFPNMLQEAIR 120

DB 289 KWPFGCKYLLBEKGHEYNINHLTRSLGALVQTKTKPSLTKRISDTIFPNMLQEAIR 348

QY 121 MGDFDKVKKIMEERITSGSNKYTLLEVADLVSAQKDTENELNQTSLQREISPEEPL 180

DB 349 MGDFDKVKKIMEERITSGSNKYTLLEVADLVSAQKDTENELNQTSLQREISPEEPL 408

QY 181 RRLQEKIKICKMDRYIAVVFIPCGHLVTCCKCAEAVDRCPMCSAVIDEKQVEMS 236

DB 409 RRLQEKIKICKMDRYIAVVFIPCGHLVTCCKCAEAVDRCPMCSAVIDEKQVEMS 464

RESULT 5

AAE00366 ID AAE00366 standard; Protein; 236 AA.

XX AAE00366;

DT 19-JUN-2001 (first entry)

DE Chimpanzee IAP-like protein-2 (IIP-2) with TGFbetar modulating activity.

XX Chimpanzee; inhibitor of apoptosis; IAP-like protein-2; IIP-2;

KW transforming growth factor beta receptor; TGFbetar;

KW c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;

KW cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;

KW T-cell acute lymphoblastic leukaemia; neurodegenerative disease;

KW retinal degeneration; hyperferritinemia-catatract syndrome; cancer;

KW autoimmune disease; diabetes; multiple sclerosis; cytosstatic.

XX Pan troglodytes.

XX MO200123568-A2.

XX 05-APR-2001.

XX 29-SEP-2000; 2000MO-US26735.

XX 30-SEP-1999; 99US-0157169.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Duckett C, Mir SS;

XX MPI: 2001-258135/26.

XX DR N-PSDB; AAD03582.

PT Inhibitors of apoptosis proteins designated IIP-2 and IIP-3 with
 PT transforming growth factor beta receptor modulating activity, and the
 PT nucleic acids that encode them, useful for treating, e.g. diabetes and
 PT multiple sclerosis -
 PS Claim 1; Fig 2; 108pp; English.

XX The present sequence is chimpanzee inhibitor of apoptosis (IAP)-like
 CC protein-2 (IIP-2). IIP-2 comprises a single amino-terminal domain
 CC known as baculovirus IAP repeat (BIR), followed by a spacer region and a
 CC carboxy-terminal ring finger domain. It interacts with transforming
 CC growth factor beta receptor (TGFbetar) and modulates TGFbetar activity.
 CC It also potentially inhibits apoptosis induced by overexpression of Bax or
 CC by Caspase-9 and Apaf-1. It also activates c-Jun N-terminal kinase (JNK)
 CC activity. IIP-2 is used in the area of genetic testing for predisposition
 CC to diseases, such as cone-rod retinal dystrophy-2, retinitis pigmentosa,
 CC glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer
 CC and hyperferritinemia-catatract syndrome owing to an IIP-2 deletion or
 CC mutation. The IIP is also used in the treatment of diseases associated
 CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,
 CC diabetes and multiple sclerosis and neurodegenerative diseases including
 CC retinal degeneration. The IIP-2 gene is also used in gene therapy for
 CC treating patients suffering from IIP-2 gene deletions or mutations.

XX Sequence 236 AA:

Query Match 98.2%; Score 1241; DB 22; Length 236;

Best Local Similarity 97.9%; Pred. No. 2.3e-117;

Matches 231; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTGEARLITFGTWMYVSNKEQLARAGFYAIGDEKVCFCGCGGLANMKPKEDPWEQHA 60

DB 1 MTGEARLITFGTWMYVSNKEQLARAGFYAIGDEKVCFCGCGGLANMKPKEDPWEQHA 60

QY 61 KWPFGCKYLLBEKGHEYNINHLTRSLGALVQTKTKPSLTKRISDTIFPNMLQEAIR 120

DB 61 KWPFGCKYLLBEKGHEYNINHLTRSLGALVQTKTKPSLTKRISDTIFPNMLQEAIR 120

QY 121 MGDFDKVKKIMEERITSGSNKYTLLEVADLVSAQKDTENELNQTSLQREISPEEPL 180

DB 121 MGDFDKVKKIMEERITSGSNKYTLLEVADLVSAQKDTENELNQTSLQREISPEEPL 180

QY 181 RRLQEKIKICKMDRYIAVVFIPCGHLVTCCKCAEAVDRCPMCSAVIDEKQVEMS 236

DB 181 RRLQEKIKICKMDRYIAVVFIPCGHLVTCCKCAEAVDRCPMCSAVIDEKQVEMS 236

RESULT 6

AAE00367 ID AAE00367 standard; Protein; 236 AA.

XX AAE00367;

DT 19-JUN-2001 (first entry)

DE Gorilla IAP-like protein-2 (IIP-2) with TGFbetar modulating activity.

XX Gorilla; inhibitor of apoptosis; IAP-like protein-2; IIP-2;

KW transforming growth factor beta receptor; TGFbetar; cytosstatic;

KW c-Jun N-terminal kinase; JNK; gene therapy; glutaricaciduria;

KW cone-rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer;

KW T-cell acute lymphoblastic leukaemia; neurodegenerative disease;

KW retinal degeneration; hyperferritinemia-catatract syndrome; cancer;

XX autoimmune disease; diabetes; multiple sclerosis.

XX Gorilla gorilla.

XX MO200123568-A2.

XX 05-APR-2001.

XX 29-SEP-2000; 2000MO-US26735.

QY 181 RRLQEKLCIKCMDRYIAVVFIPCGHLVTCQKCAEAVDRCPMCSAVIDFKORVEMS 236
 DB 442 RRLQEKLCIKCMDRNIAIVFVPCGHLVTCQKCAEAVDRCPMCSAVITFKOKIEMS 497

RESULT 10
 ID AAY99985 standard; Protein: 497 AA.
 AC AAY99985;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human X-linked inhibitor of apoptosis.
 XX
 KW X-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880;
 KM antisense; antiinflammatory; cytostatic; tumour.
 XX
 OS Homo sapiens.
 XX
 PN US6087173-A.
 PD 11-JUL-2000.
 XX
 PE 09-SEP-1999; 99US-0392580.
 PR 09-SEP-1999; 99US-0392580.
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Cowsett LM, Ackermann EJ;
 DR WPI: 2000-498201/44.
 DR N-PSDB; AAA64901.

PT Antisense compound useful for research reagents, diagnostics,
 PT prophylaxis and for treating disorders associated with X-linked
 PT inhibitor of apoptosis, modulates expression of X-linked inhibitor of
 PT apoptosis -
 XX
 PS Example 13; Column 43-48; 33pp; English.

CC The present invention relates to antisense oligonucleotides designed to
 CC inhibit expression of the human X-linked inhibitor of apoptosis
 CC (the present sequence). Modified phosphorothioate 2'-MOE
 CC oligonucleotides are more effective inhibitors than unmodified
 CC oligonucleotides. The oligonucleotides may be used to inhibit X-linked
 CC inhibitor of apoptosis expression in cells and tissues in vitro. The
 CC oligonucleotides are also useful for treating animals or humans, prone
 CC to a disease associated with X-linked inhibitor of apoptosis. The
 CC oligonucleotides may also be used prophylactically to prevent
 CC infection, inflammation or tumour formation.
 CC
 SQ Sequence 497 AA;

Query Match 83.2%; Score 1052; DB 21; Length 497;
 Best Local Similarity 80.1%; Pred. No. 9, 3e-98;
 Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

QY 1 MTGFEARLITFGTMMYSYNNKQALRAGFYAIGQEDKVOCFHGGGLANKPKEDPWEQHA 60
 DB 262 MADFEARLITFGTMMYSYNNKQALRAGFYAIGQEDKVOCFHGGGLANKPKEDPWEQHA 321

QY 61 KMYPGCKYLLEBKGEHYNNHILFRSLGALVQTKRPSLTKRISDITFPNMLQPAIR 120
 DB 322 KMYPGCKYLLEBKGEHYNNHILFRSLGALVQTKRPSLTKRISDITFPNMLQPAIR 381

QY 121 MGPFKDKVKIMEEKIOTSGSNYKTLLEVYADLVNKKQKSDSSQTSIQKEISTEOL 180
 DB 382 MGPFKDKVKIMEEKIOTSGSNYKTLLEVYADLVNKKQKSDSSQTSIQKEISTEOL 441

QY 181 RRLQEKLCIKCMDRYIAVVFIPCGHLVTCQKCAEAVDRCPMCSAVIDFKORVEMS 236

DB 442 RRLQEKLCIKCMDRNIAIVFVPCGHLVTCQKCAEAVDRCPMCSAVITFKOKIEMS 497

RESULT 11
 ID ABG65663 standard; Protein: 497 AA.
 AC ABG65663;
 XX
 DT 26-AUG-2002 (first entry)
 XX
 DE Human inhibitor of apoptosis, XIAP.
 XX
 KW Human; antisense; inhibitor of apoptosis; HIAPI; HIAPI2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200226968-A2.
 PD 04-APR-2002.
 XX
 PE 27-SEP-2001; 2001WO-CA01379.
 PR 28-SEP-2000; 2000US-0672717.
 PA (UYOT-) UNIV OTTAWA.
 PA (ABGE-) ABERG THERAPEUTICS INC.
 XX
 PI Korneluk RG, Iacasse E, Baird S, Holcik M, Young S;
 DR WPI: 2002-479562/51.
 DR N-PSDB; ABK93869.

PT Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases -
 XX
 PS Example 12; Fig 1; 135pp; English.

CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAPI or HIAPI2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC protein sequence.
 CC
 SQ Sequence 497 AA;

Query Match 83.2%; Score 1052; DB 23; Length 497;
 Best Local Similarity 80.1%; Pred. No. 9, 3e-98;
 Matches 189; Conservative 25; Mismatches 22; Indels 0; Gaps 0;

QY 1 MTGFEARLITFGTMMYSYNNKQALRAGFYAIGQEDKVOCFHGGGLANKPKEDPWEQHA 60
 DB 262 MADFEARLITFGTMMYSYNNKQALRAGFYAIGQEDKVOCFHGGGLANKPKEDPWEQHA 321

```

QY 61 KWPCKYLLLEKGEHYNNIHLFRSLGALVOTTKTPSLTKRISDTIFPNPMLOEAI 120
DB 322 KWPCKYLLLEKGEHYNNIHLFRSLGALVOTTKTPSLTKRISDTIFPNPMLOEAI 381
QY 121 MGFDKDVKKIMEERIQTSNGSKYLEVYADLVSAOKDTENELNQTSLQREISPEEPL 180
DB 382 MGFSFKDIKKIMEERIQTSNGSKYLEVYADLVSAOKDTENELNQTSLQREISPEEPL 441
QY 181 RLQOEKLCIKCMRDRIYAVVFIPGCHLYTCCKCAEAVDRCPCMSAVIDFKQRYEVS 236
DB 442 RLQOEKLCIKCMRDRIYAVVFIPGCHLYTCCKCAEAVDRCPCMSAVIDFKQRYEVS 497

RESULT 12
AAV59451
ID AAV59451 standard; Protein; 497 AA.
XX
AC AAV59451;
XX
DT 24-MAR-2000 (first entry)
XX
DE Human XIAP protein sequence.
XX
KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
KW transforming growth factor-beta activated kinase 1; monocyte migration;
KW TAK1 binding protein 1; extracellular matrix protein production;
KW cell growth inhibitor; beta-amyloid protein deposition;
KW immunosuppression; Transforming growth factor-beta.
XX
OS Homo sapiens.
XX
PN JP1326328-A.
XX
PD 26-NOV-1999.
XX
PF 13-MAY-1998; 98JP-0130378.
XX
PR 13-MAY-1998; 98JP-0130378.
XX
PA (MATSU) MATSUMOTO K.
XX
DR MPI: 2000-078337/07.
XX
N-PSDB: AAZ48862.
XX
PT Screening a substance which inhibits combination of the X-linked
PT inhibitor of apoptosis protein -
XX
PS Claim 3; Page 28-30; 43pp; Japanese.
XX
CC This sequence represents the human XIAP protein.
CC The invention relates to a method for screening a substance inhibiting
CC the formation of a complex between XIAP and TAB1, in which X-linked
CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta
CC activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be
CC tested are contacted with each other and then the presence or formation
CC of a complex between XIAP and TAB1 is detected. The substance can be used
CC as a drug for extracellular matrix protein production enhancement, cell
CC growth inhibition, monocyte migration, physiologically active substance
CC induction, immunosuppression, and beta-amyloid protein deposition. A
CC substance inhibiting the formation of a complex between TAB1 and XIAP as
CC well as between XIAP and TGF-beta (Transforming growth factor-beta) type
CC I and/or type II receptor is useful as a drug.
XX
SQ Sequence 497 AA;
QY Query Match 83.0%; Score 1049; DB 21; Length 497;
DB Best Local Similarity 80.1%; Pred. No. 1.9e-97;
Matches 189; Conservative 24; Mismatches 23; Indels 0; Gaps 0;
QY 1 MTGFEARLFTFTGMYSVNKEQLARAGFYAIGQEDKVCFCGGGLANMKPKEDPWEOHA 60
DB 262 MADYEARELFTFTGMYSVNKEQLARAGFYAIGQEDKVCFCGGGLANMKPKEDPWEOHA 321

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QY 61 KWPCKYLLLEKGEHYNNIHLFRSLGALVOTTKTPSLTKRISDTIFPNPMLOEAI 120
DB 322 KWPCKYLLLEKGEHYNNIHLFRSLGALVOTTKTPSLTKRISDTIFPNPMLOEAI 381
QY 121 MGFDKDVKKIMEERIQTSNGSKYLEVYADLVSAOKDTENELNQTSLQREISPEEPL 180
DB 382 MGFSFKDIKKIMEERIQTSNGSKYLEVYADLVSAOKDTENELNQTSLQREISPEEPL 441
QY 181 RLQOEKLCIKCMRDRIYAVVFIPGCHLYTCCKCAEAVDRCPCMSAVIDFKQRYEVS 236
DB 442 RLQOEKLCIKCMRDRIYAVVFIPGCHLYTCCKCAEAVDRCPCMSAVIDFKQRYEVS 497

RESULT 13
AAW19745
ID AAW19745 standard; Protein; 496 AA.
XX
AC AAW19745;
XX
DT 16-SEP-1997 (first entry)
XX
DE Mouse inhibitor of apoptosis protein homologue MIRA.
XX
KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIRA;
KW degenerative disease; infectious disease; autoimmune disease;
KW cancer; therapy; diagnosis.
XX
OS Mus musculus.
XX
FH Key
FH Region Location/Qualifiers
FH FT 26..93
FH FT /label= BIR
FH FT 163..230
FH FT /label= BIR
FH FT 264..330
FH FT /label= BIR
FH FT 448..485
FH FT /label= RING_finger
XX
PN M09723501-A1.
XX
PD 03-JUL-1997.
XX
PF 20-DEC-1996; 96MO-AU00827.
XX
PR 22-DEC-1995; 95AU-0007275.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Vaux DL;
XX
DR MPI: 1997-350966/32.
XX
N-PSDB: AAW272710.
XX
PT Isolated protein homologues of viral inhibitors of apoptosis - used
PT to modulate apoptosis for treatment of degenerative, infectious or
PT autoimmune diseases and cancer
XX
PS Claim 7; Page 44-47; 136pp; English.
XX
CC Mammalian IAP homologue A (MIRA) (AAW19745) is a murine homologue of
CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
CC sequence was deduced from a cDNA clone (see also AAW272710) isolated
CC from a mouse liver cDNA library on the basis of homology to Orgyia
CC pseudotsuguta polyhedrosis virus IAP BIR and RING finger amino acid
CC motifs (see also AAW19744). IAP homologues (see also AAW19746-52) and
CC their derivatives and chemical analogues can be used in methods for
CC modulating apoptosis in animal cells, specifically for treatment,
CC by inhibition, of degenerative and infectious disease or, by
CC promotion, of cancer and autoimmune disease.
XX
SQ Sequence 496 AA;

```


XX This sequence is the murine XIAP protein, which is a inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors.

XX
 SQ Sequence 496 AA;

Query Match 78.2%; Score 989; DB 19; Length 496;

Best Local Similarity 75.8%; Pred. No. 2, 2e-91;
 Matches 179; Conservative 27; Mismatches 30; Indels 0; Gaps 0;

QY 1 MTGYEARLITFGTWMYVYNKEQLARAGFYAIGQEDRVQCFHCGGGLANMKPKEDPWEQHA 60
 Db 261 MAEYEARIVTFGTWYVYNKEQLARAGFYALGEGDKVCFHCGGGLTDMKPSDEPDQHA 320
 QY 61 KMYRCKTLLEKKGHEYNHILTRSLGALVQTKKPSLTRISDTIFPNMLOEAIR 120
 Db 321 KQYPCCKYLDEKGGEGYINNHLTHPLESLGRTAEKTPPLTKKIDTIFONPMVOEAIR 380
 QY 121 MGFDKDYKIMEERIQTSGSNYKTLLEVAVADIVSAQKDTTENELNOTSLQREISPEEPL 180
 Db 381 MGFSKDLKKTMEKIQTSGLSYLSLEVLADIVSAQKDNTEDESQTSLOKDISTEEQL 440
 QY 181 RRLQEKILCKICMDRIYAVFIIPCGHLVTCCKCAEAVDRCPMCSAVIDFKORVPM 236
 Db 441 RRLQEKILCKICMDRNIYAVFPCGHLATCKCAEAVDRCPMCTVITFNOKIFMS 496

Search completed: June 19, 2003, 10:10:34
 Job time : 37 secs

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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:07:04 ; Search time 18 Seconds

(without alignments)
1260.429 Million cell updates/sec

Title: US-10-024-433-2

Perfect score: 1264

Sequence: 1 MTGEARLITFGTMYSVNK.....VDRCPMCSAVIDEKQVEMWS 236

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : PIR_73:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1049	83.0	497	2	S69544
2	466.5	36.9	604	2	S68449
3	454.5	36.0	618	2	S68450
4	427	33.8	358	2	JC5964
5	402.5	31.8	497	2	S69545
6	400	31.6	496	2	S68452
7	373.5	29.5	298	2	JC7566
8	314.5	24.9	275	2	A45679
9	312.5	24.7	268	2	T10304
10	312.5	24.7	268	2	A53989
11	222.5	17.6	1447	2	T42628
12	209.5	16.6	1232	2	A55478
13	205	16.2	208	2	T03183
14	200.5	15.9	155	2	T30489
15	193.5	15.3	150	2	T28409
16	192	15.2	292	2	T41772
17	182	14.4	275	2	T10310
18	179	14.2	286	2	D36828
19	165.5	13.1	249	2	H72858
20	161.5	12.8	249	2	T41814
21	147.5	11.7	316	2	T32659
22	144	11.4	383	2	F96582
23	143	11.3	263	2	T22135
24	139	11.0	711	2	C84767
25	133	10.5	329	2	T28403
26	128	10.1	4845	2	T31067
27	127.5	10.1	864	2	T01393
28	126	10.0	115	2	S77736
29	125	9.9	2	2	B96664

ALIGNMENTS

30	124.5	9.8	347	2	T01044	hypothetical prote
31	122	9.7	785	2	T00474	hypothetical prote
32	120.5	9.5	823	2	D86165	protein F15K9.3 [i
33	119.5	9.5	943	2	S68824	rbg protein, cyto
34	119	9.4	936	2	E71405	probable ankryn -
35	117	9.3	673	2	T21007	hypothetical prote
36	114.5	9.1	285	2	T05777	hypothetical prote
37	112.5	8.9	234	2	T30427	probable apoptosis
38	111	8.8	433	2	JC7678	RING finger protei
39	110.5	8.7	780	2	T31548	hypothetical prote
40	110	8.7	204	2	T01447	hypothetical prote
41	110	8.7	582	2	S57722	sll-1 protein - Ca
42	110	8.7	585	2	T29654	hypothetical prote
43	109.5	8.7	428	2	T48167	hypothetical prote
44	109.5	8.7	489	2	S71955	MDM2-like p53-bind
45	108.5	8.6	614	2	S42526	finger protein unk

RESULT 1

S69544
apoptosis inhibitor IAP homolog - human
C:Species: Homo sapiens (man)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: S69544; S68451
R:Dickelt, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gillfillan, E.M.B. J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and
A:Reference number: S69544; MUID:96256286; PMID:8654366
A:Accession: S69544
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DCC>
A:Cross-references: EMBL:U32974; NID:91016687; PIDN:AAC50518.1; PID:91016688
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chertton-Horvat, G.; Faraha Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68451
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-161, 'C', 163-422, 'O', 424-497 <LIS>
A:Cross-references: EMBL:U45880; NID:91184319; PIDN:AAC50373.1; PID:91184320
C:Genetics:
A:Gene: IIP
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

Query Match 83.0%; Score 1049; DB 2; Length 497;

Best Local Similarity 80.1%; Pred. No. 1e-75;
Matches 189; Conservative 24; Mismatches 23; Indels 0; Gaps 0;

QY	1	MTGEARLITFGTMYSVNKQRLARAGFYALGQEDKVCQFCGGLAMKPKEDPWEQHA	60
DB	262	MADYEARIFFGTWYSVNEKQLARAGFYALGEGDKVACFCGGLTWMKPSDEWEQHA	321
QY	61	KWYFGCYLLEKEHEVNNIHLTRSEGLAVQTKRPSLTKRISDTIFPMLQEAR	120
DB	322	KWYFGCYLLEKQKOEYNNIHLTHSLSECLVTRTEKPSLTKRISDTIFPMLQEAR	381
DB	382	MGFSFKIKRIMEKIOISGSNYKSLVADVADVAQDSMPDESSQSLQKEISTEQL	441
QY	121	MGFDKVKYKIMEIRIQTSGSNYKTLVADVADVAQDTEENELNQSLOREISDEPL	180
QY	181	RLQEEKLKTCQMRVAVVFIPOGHVATCKQCAAVVRCPCMSAVIDFKQVEMWS	236
DB	442	RLQEEKLKTCQMRVAVVFIPOGHVATCKQCAAVVRCPCMSAVIDFKQVEMWS	497

apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S69545
 R:Unckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gillfillan, M.C.
 EMO J. 15, 2685-2694, 1996
 A:Title: A conserved family of cellular genes related to the baculovirus iap gene and er
 A:Reference number: S69544; MUID:96256286; PMID:8654366
 A:Accession: S69545
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-497 <DUC>
 A:Cross-references: EMBL:U32373; NID:g1019116; PIDN:AAC47155.1; PID:g1019117
 C:Genetics:
 A:Gene: i1p
 C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
 F:446-490/Domain: RING finger homology <RNG>

Query Match 31.8%; Score 402.5; DB 2; Length 497;
 Best Local Similarity 30.9%; Pred. No. 2.5e-24;
 Matches 89; Conservative 46; Mismatches 94; Indels 59; Gaps 4;
 QY 5 EARLITFGTWMYS--VNKEQLARAGFYAIGDEKVOCFHGGGGLANMKPKEDPWEQAKW 62
 DB 213 DARLRFETMPISNIQPSALAGLYYKIGQVRCFHCNIGLSWQKEDPEWEHAKW 272
 QY 63 YPGCKYLEEGHEYYNNIHLRSLGALVQTKTPSLTKRISDTIFPNMQLQEAIRMG 122
 DB 273 SPKCOFVLLAKGPAVSEVLAATAANASSPAPATPILQ---ADVLMDEAPAKAELALG 329
 QY 123 PFKDYKKTMEERIORGSNYKLEVL----- 149
 DB 330 IGGVVRNAIORKLSSGCAFTLDELHDIFDDAGAGADWRCASREPSAPFIEPCQAT 389
 QY 150 -----VADVSAOKDTTENELNQTSLQREI-----SPEEPLRLQOEK 188
 DB 390 SKAASVPPIVADSIAPKPOAAEAVANSIKITDEIQKMSVATPNCNLSLEENRQLKDAR 449
 QY 189 CKICMDRIYAVFIPIGCHLVYCKQCAEAVDRCPMCSAVIDEKKORVPM 236
 DB 450 CVCCLDEEVGVVFLPCGHLATCNCAPSVANCPMCRADIKGFVTFELS 497

RESULT 6
 S68452
 apoptosis inhibitor diap - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Nov-2000
 C:Accession: S68452; S78528
 R:Lisbon, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
 Nature 379, 349-353, 1996
 A:Title: Suppression of apoptosis in mammalian cells by Nalp and a related family of IAP
 A:Reference number: A56182; MUID:96149249; PMID:8552191
 A:Accession: S68452
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-496 <LIS>
 A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
 R:Baird, S.D.
 submitted to the EMBL Data Library, January 1996
 A:Accession: S78528
 A:Molecule type: mRNA
 A:Residues: 1-36, 'AT', '37', 'K', '39', 'L', '41-44', 'H', '46-58', 'Q', '60-612', 'A', '414-427', 'A', '429-496'
 A:Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0015247
 C:Function:
 A:Description: apoptotic suppressor
 C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
 C:Keywords: apoptosis; zinc finger
 F:445-489/Domain: RING finger homology <RNG>

Query Match 31.6%; Score 400; DB 2; Length 496;
 Best Local Similarity 30.8%; Pred. No. 3.9e-24;
 Matches 89; Conservative 46; Mismatches 94; Indels 60; Gaps 4;
 QY 5 EARLITFGTWMYS--VNKEQLARAGFYAIGDEKVOCFHGGGGLANMKPKEDPWEQAKW 62
 DB 211 DARLRFETMPISNIQPSALAGLYYKIGQVRCFHCNIGLSWQKEDPEWEHAKW 270
 QY 63 YPGCKYLEEGHEYYNNIHLRSLGALVQTKTPSLTKRISDTIFPNMQLQEAIRMG 122
 DB 271 SPKCOFVLLAKGPAVSEVLAATAANASSPAPATPILQ---ADVLMDEAPAKAELALG 327
 QY 123 PFKDYKKTMEERIORGSNYKLEVL----- 149
 DB 328 IGGVVRNAIORKLSSGCAFTLDELHDIFDDAGAGALEVREPPSPAPFIEPCQAT 387
 QY 150 -----VADVSAOKDTTENELNQTSLQREI-----SPEEPLRLQOEK 187
 DB 388 SKAASVPPIVADSIAPKPOAAEAVANSIKITDEIQKMSVATPNCNLSLEENRQLKDAR 447
 QY 188 CKICMDRIYAVFIPIGCHLVYCKQCAEAVDRCPMCSAVIDEKKORVPM 236
 DB 448 LCKVCLDEEVGVVFLPCGHLATCNCAPSVANCPMCRADIKGFVTFELS 496

RESULT 7
 JC7568
 kidney inhibitor of apoptosis protein - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
 C:Accession: JC7568
 R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.
 Biochem. Biophys. Res. Commun. 279, 820-831, 2000
 A:Title: Klap, a novel member of the inhibitor of apoptosis protein family.
 A:Reference number: JC7568; MUID:21092523; PMID:11162435
 A:Accession: JC7568
 A:Contents: Fetal kidney
 A:Molecule type: mRNA
 A:Residues: 1-298 <LIN>
 C:Comment: This protein, a new member of the inhibitor of apoptosis protein family, p

Query Match 29.5%; Score 373.5; DB 2; Length 298;
 Best Local Similarity 32.2%; Pred. No. 2.7e-22;
 Matches 82; Conservative 42; Mismatches 72; Indels 59; Gaps 9;
 QY 1 MTGYEARLITFGTWMYS--VNKEQLARAGFYAIGDEKVOCFHGGGGLANMKPKEDPWEQ 58
 DB 84 MGEELRLASFYDWPLTALEVPPELAAAGFFHGHODKRCFCYGLQSWKRGDPPWE 143
 QY 59 HAKWPGCKYLEEGHEYYNNIHLRSLGALVQTKTPSLTKRISDTI-----F 110
 DB 144 HAKWPGCKYLEEGHEYYNNIHLRSLGALVQTKTPSLTKRISDTI-----F 110
 QY 111 PPMQLQEAIRMGFDPKDYKKTMEERIORGSNYKLEVLVADVSAOKDTTENELNQTSL 170
 DB 202 PTPR-----REVQSESAOEPGG-----VSPAEA 224
 QY 171 QRE-----ISP-----EPLRLQOEKCKICMDRIYAVFIPIGCHLVYCKQCAEAVDRCP 221
 DB 225 QRAMVVLPPGARDVDAOLRLQOEKTCVCLDRAVSIVFPGHLY-CAECAPGLQDC 283
 QY 222 MCSAVIDEKKORVPM 236
 DB 284 ICRAPVRSRVRTFLS 298

RESULT 8
 A45679

inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV

C:Species: Cydia pomonella granulosis virus CpGV

C:Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000

C:Accession: A45679

R:Clcock, N.E.; Clem, R.J.; Miller, L.K.

J. Virol. 67, 2168-2174, 1993

A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.

A:Reference number: A45679; MUID:93188168; PMID:8445726

A:Accession: A45679

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-275 <GB>

A:Cross-references: GB:I05494; NID:q289583; PIDN:AAA4835.1; PID:9289584

A>Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBIPI:127015)

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 24.9%; Score 314.5; DB 2; Length 275;

Best Local Similarity 27.9%; Pred. No. 1.2e-17;

Matches 65; Conservative 38; Mismatches 61; Indels 69; Gaps 5;

6 ARLLFTGTMYSVKN--EQIARAGFYALIGEDKVCQCHGCGGLANMKPKEDPWEQHAHMY 63

110 AAVKSFHNPCKQRPQEQADAGFFYTGVDNKCFCGDLKDWEPEDVPEQHVHWF 169

64 PGCKYLLEKGEHYINNHLTRSLGALVQTTKTPSLTKRISDTIFPNMLOEALRMGF 123

170 DKCAVQVLYKGRDY----- 183

124 DKDYAKKIMEIRIOTSGSNYKTELVADIVSAOKDTTENELNOSTLOREISPEEPLRL 183

184 ---VQKVTAEACVLPGEN-----TTVSTAPASE-PIPEKTIKE-----PQV 222

184 QEEKLCKICMDRYIAVVFIPCGHLVTCQCAEAVIDRCPMCSAVIDEQRVMS 236

223 ESKLCKICVVEICVCFPCGHVAVACAKALSDCKPMCKRIYTVLKVIFS 275

Db

RESULT 9

T10304

Inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus

C:Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OPMNV

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000

C:Accession: T10304

R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohmann, G.F.

Virol. 229, 381-399, 1997

A:Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis

A:Reference number: Z17011; MUID:97271300; PMID:9126251

A:Accession: T10304

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-268 <AHR>

A:Cross-references: EMBL:U75930; NID:92934903; PIDN:AAC59034.1; PID:91911281

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

F:217-261/Domain: RING finger homology <RRN>

Query Match 24.7%; Score 312.5; DB 2; Length 268;

Best Local Similarity 27.7%; Pred. No. 1.7e-17;

Matches 64; Conservative 31; Mismatches 57; Indels 79; Gaps 4;

6 ARLLFTGTMYSVKN--EQIARAGFYALIGEDKVCQCHGCGGLANMKPKEDPWEQHAHMY 63

113 ARLLFTFAEMPRGLKQREPELEAGFFYTGQDKTRCCDGLKDWEPDDAQQOAHARY 172

64 PGCKYLLEKGEHYINNHLTRSLGALVQTTKTPSLTKRISDTIFPNMLOEALRMGF 123

173 DKCEYVLLVGRDVRV---MTACVVRADNDEPHIER----- 208

124 DKDYAKKIMEIRIOTSGSNYKTELVADIVSAOKDTTENELNOSTLOREISPEEPLRL 183

209 -----PAVEAEVAD----- 217

184 QEEKLCKICMDRYIAVVFIPCGHLVTCQCAEAVIDRCPMCSAVIDEQRVMS 234

220 WEPKCEFLQSKSPSEIR--QYVQSYEGFLHTGHEFVNSWRRELPMVSAYCNDSEVAN 277

Db 218 --DRLCKICGAECTVCFVPCGHVAVACGKACAGYTTCPVCRQGLDKAVRMV 266

RESULT 10

A53989

apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis

C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OPMNV

C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Sep-2000

C:Accession: A53989

R:Birdnam, M.J.; Clem, R.J.; Miller, L.K.

J. Virol. 68, 2521-2528, 1994

A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a po

A:Reference number: A53989; MUID:94187094; PMID:8139034

A:Accession: A53989

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-268 <BIR>

A:Cross-references: GB:I22564; NID:9456111; PIDN:AA02610.1; PID:9456114

A>Note: authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50 as

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

F:217-261/Domain: RING finger homology <RRN>

Query Match 24.7%; Score 312.5; DB 2; Length 268;

Best Local Similarity 27.7%; Pred. No. 1.7e-17;

Matches 64; Conservative 31; Mismatches 57; Indels 79; Gaps 4;

6 ARLLFTGTMYSVKN--EQIARAGFYALIGEDKVCQCHGCGGLANMKPKEDPWEQHAHMY 63

113 ARLLFTFAEMPRGLKQREPELEAGFFYTGQDKTRCCDGLKDWEPDDAQQOAHARY 172

64 PGCKYLLEKGEHYINNHLTRSLGALVQTTKTPSLTKRISDTIFPNMLOEALRMGF 123

173 DKCEYVLLVGRDVRV---MTACVVRADNDEPHIER----- 208

124 DKDYAKKIMEIRIOTSGSNYKTELVADIVSAOKDTTENELNOSTLOREISPEEPLRL 183

209 -----PAVEAEVAD----- 217

184 QEEKLCKICMDRYIAVVFIPCGHLVTCQCAEAVIDRCPMCSAVIDEQRVMS 234

218 --DRLCKICGAECTVCFVPCGHVAVACGKACAGYTTCPVCRQGLDKAVRMV 266

Db

RESULT 11

T42628

neuronal apoptosis inhibitory protein 2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C:Accession: T42628

R:Faraghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.

Mamm. Genome 10, 761-763, 1999

A:Title: CDNA cloning and the 5' genomic organization of Nalp2, a candidate gene for m

A:Reference number: Z22179; MUID:99315342; PMID:10384056

A:Accession: T42628

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1447 <YAR>

A:Cross-references: EMBL:AF102871; NID:93860228; PID:93860229; PIDN:AAC73002.1

A:Gene: Nalp2

Query Match 17.6%; Score 222.5; DB 2; Length 1447;

Best Local Similarity 37.0%; Pred. No. 1.8e-09;

Matches 50; Conservative 22; Mismatches 44; Indels 19; Gaps 5;

5 EARLLTGTWY--MYSVKNEDLARAGFYALIGEDKVCQCHGCGGLANMKPKEDPWEQHAHMY 61

160 EARLESFEDWPFYAHGTSRVALSAGFVFTGKRDTVQCCGGLANMKWEGDDPMKEHAK 219

62 WYPCCKYLLEKGEHYINNHLTRSLGALVQTTKTPSLTKRISDTIFPN 112

220 WEPKCEFLQSKSPSEIR--QYVQSYEGFLHTGHEFVNSWRRELPMVSAYCNDSEVAN 277

OY 113 PMLQEAIRMGDFPKD 127
 Db 278 ----EELRLMD-TFKD 287

RESULT 12

A53478

neural apoptosis inhibitory protein - human

N:Alternate names: NAIP

C:Species: Homo sapiens (man)

C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001

C:Accession: A53478

R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuttler, G.; Yarahni, Z.; Farahani, R.; Baird, S.
 d, T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; Mackenzie, A.
 Cell 80, 167-178, 1995

A:Title: The gene for neural apoptosis inhibitory protein is partially deleted in indi

A:Reference number: A53478; MUID:95112344; PMID:7815013

A:Accession: A53478

A:Molecule type: mRNA

A:Residues: 1-1232 <ROY>

A:Cross-references: GB:U19251

C:Genetics:

A:Gene: GDB:SMA6; SMA

A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300

A:Map position: 5q12.2-q13

C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prot

F:94-110/Domain: transmembrane #status predicted <TM1>

F:470-477/Region: nucleotide-binding motif A (P-loop)

F:479-496/Domain: transmembrane #status predicted <TM2>

F:476/Binding site: ATP (Lys) #status predicted

F:518,632,823,923,1035/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 16.6%; Score 209.5; DB 2; Length 1232;

Best Local Similarity 34.8%; Pred. No. 1.6e-08;

Matches 47; Conservative 25; Mismatches 44; Indels 19; Gaps 5;

OY 5 EARLITFTGWTW---SYNKEQLARAGFYAIGQEDKVCFCFGGGLANMKPKEDPWEQAK 61

Db 160 EARLAFRMRPFVVGQSPCLVSGFVFGKQDTVOCCGCLGNWEEDDDPKKEHAK 219

OY 62 WYPCCKYLLEKGEHYINNIHLTRSLGALVOT-----TKTSLTRISDTPPN 112

Db 220 WYPCCKFLSKSESELT--QYTSYKGFVDITGEHFVNSWVQRELPWASAYCNDISF-- 275

OY 113 PMLQEAIRMGDFPKD 127

Db 276 --AYEELRLD-SPKD 287

RESULT 13

T03183

Probable apoptosis inhibitor - Chilo iridescent virus

C:Species: Chilo iridescent virus

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Sep-2000

C:Accession: T03183

R:Bahr, U.; Tidon, C.A.; Darat, G.

Virus Genes 15, 233-245, 1997

A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101

A:Reference number: Z14834; MUID:98141693; PMID:9482589

A:Accession: T03183

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-208 <BAH>

A:Cross-references: EMBL:AF003534; MID:92738385; PIDN:AA594481.1; PID:92738454

A:Suprafamily: RING finger homology

F:159-202/Domain: RING finger homology <RRN>

Query Match 16.2%; Score 205; DB 2; Length 208;

Best Local Similarity 26.6%; Pred. No. 4.3e-09;

Matches 59; Conservative 27; Mismatches 72; Indels 64; Gaps 7;

OY 4 YEARLITFTGWTW---SYNKEQLARAGFYAIGQEDKVCFCFGGGLANMKPKEDPWEQAK 61

Db 159 --AYEELRLD-SPKD 287

RESULT 14

T30489

apoptosis inhibitor - Lymantria dispar nuclear polyhedrosis virus

C:Species: Lymantria dispar nuclear polyhedrosis virus; LdMNPV

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T30489

R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; R

Virology 253, 17-34, 1999

A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria

A:Reference number: Z20836; MUID:99124785; PMID:9887315

A:Accession: T30489

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-155 <KUZ>

A:Cross-references: EMBL:AF081810; PIDN:AACT0325.1

Query Match 15.9%; Score 200.5; DB 2; Length 155;

Best Local Similarity 22.8%; Pred. No. 6.8e-09;

Matches 54; Conservative 30; Mismatches 68; Indels 85; Gaps 6;

OY 1 MTGYEARLITFTGWTW---SYNKEQLARAGFYAIGQEDKVCFCFGGGLANMKPKEDPWEQ 58

Db 1 MDERRLRLSFRMSAVDAPAPALAHAGTYCANRQDFVCAVCHIEIGMSIGSDMSD 60

OY 59 HAKWYPCCKYLLEKGEHYINNIHLTRSLGALVOTTKKPSLTKRISDTPPNMLQEA 118

Db 61 HKRYSPACRFVCE-----LTKR---PVSP----- 81

OY 119 IMGFDFKVKKIMERIOTSGSNKYTLVADVSAQKDTTENELNOTSLOREISPEE 178

Db 82 -----ERRRDDDED-----EEDSAAE 99

OY 179 PLRLQEEKLCKICMDRYIAVVFIPCGHLVYTCQKQEAVIDRCPMSAVIDFKQRYEM 235

Db 100 PAR--GGELLCVCLDAQREIMSPCHHYVCCAPCADMDACVYCAVRAVERRVKFL 154

RESULT 15

T28409

ORF MSV248 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes ent

C:Species: Melanoplus sanguinipes entomopoxvirus

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

C:Accession: T28409

R:Alonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.

J. Virol. 73, 533-552, 1999

A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A:Reference number: Z20484; MUID:99102612; PMID:9847359

A:Accession: T28409

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-150 <AFD>

A:Cross-references: EMBL:AF063866; MID:94049647; PIDN:AACT97724.1; PID:94049764

C:Genetics:

A>Note: MSV248

Query Match 15.3%; Score 193.5; DB 2; Length 150;

Best Local Similarity 19.3%; Pred. No. 2.4e-08;

Matches 43; Conservative 26; Mismatches 51; Indels 103; Gaps 4;

```

QY 5 EARLITEGTW---MYSVKEQLARAGFYAIGQEDKVOCCFHCGGLANMKPKEDPWEQHA 60
Db 17 OSRINSYENMFIISLEFKINR--LCEAGFEYTNIGDITVCFCNGGLKIKNMLYNDPWIEHS 74
QY 61 KWPQCKYILEEKGEHYTNHILHLSLGGALVOTTKTKRISDTIFPNPMLQEAIR 120
Db 75 KMSPCNHYIIPNKGKFIN-----FAKNEKHQLLYN----- 105
QY 121 MGFEKDYKKIMEERIQTSGSNYKTLLEVADLVSAQKDTTENELNOTSLQREISPEPL 180
Db 106 ----- 105
QY 181 RRIQEEKLCKICMDRYIAVETPCGHLVTCQCAEAVDRCPWC 223
Db 106 -----CICNENNISYIILKPCGHASTCYECSSKIKYKCPVC 140

```

Search completed: June 19, 2003, 10:08:03
 Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 10:07:04 ; Search time 80 seconds
(without alignments)
607.839 Million cell updates/sec

Title: US-10-024-433-2

Perfect score: 1264
Sequence: 1 MTGFEARLITFGTWMYSVNK.....VDRCPMSAVIDKQRFVMS 236

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_trembl_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mmc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1264	100.0	236	4 Q96P09	Q96P09 homo sapien
2	1259	99.6	236	4 Q96RM5	Q96RM5 homo sapien
3	1241	98.2	236	6 Q95M72	Q95M72 pan troglod
4	1237	97.9	236	6 Q95M71	Q95M71 gorilla gor
5	1025	81.1	496	11 Q9ESF0	Q9ESF0 rattus norv
6	1015	80.3	501	11 Q9EO05	Q9EO05 rattus norv
7	1011	80.0	501	11 Q9EO04	Q9EO04 rattus norv
8	678.5	55.7	493	13 Q8UVP8	Q8UVP8 gallus gall
9	497.5	33.4	628	13 Q8UWD2	Q8UWD2 brachydanio
10	465	33.8	610	13 Q8V319	Q8V319 gallus gall
11	452.5	33.8	106	4 Q96RW6	Q96RW6 homo sapien
12	445.5	33.2	602	11 Q9ESE9	Q9ESE9 rattus norv
13	445	35.2	589	11 Q9ESB3	Q9ESB3 rattus norv
14	445	35.2	589	11 Q9OZC6	Q9OZC6 rattus norv
15	432	34.2	405	13 Q8UWH2	Q8UWH2 brachydanio
16	401	31.7	498	5 Q96U03	Q96U03 drosophila

17	376.5	29.8	280	4 Q9HAP7	Q9HAP7 homo sapien
18	373.5	29.5	298	4 Q9H2A8	Q9H2A8 homo sapien
19	373.5	29.5	298	4 Q96CA5	Q96CA5 homo sapien
20	325.5	25.8	403	5 Q8MRP9	Q8MRP9 ochlerotatu
21	325	25.7	438	5 Q9VUX5	Q9VUX5 drosophila
22	320.5	25.4	377	5 Q9NU07	Q9NU07 spodoptera
23	320	25.3	346	5 Q968R8	Q968R8 bombyx mori
24	317.5	25.1	281	12 Q9VNL8	Q9VNL8 choristoneu
25	311	24.6	379	5 Q9U492	Q9U492 trichoplusi
26	308.5	24.4	313	12 Q9J827	Q9J827 spodoptera
27	305	24.1	261	12 Q9QDS9	Q9QDS9 epiphyas po
28	305	24.1	276	12 Q89744	Q89744 dzura supp
29	300.5	23.8	402	5 Q8T621	Q8T621 aedes allop
30	289.5	22.9	264	12 Q9EN27	Q9EN27 amsacta moo
31	283.5	22.4	268	12 Q9E332	Q9E332 helioverpa
32	282	22.3	276	12 Q8OL95	Q8OL95 mamestra co
33	280.5	22.2	268	12 Q9JFT8	Q9JFT8 helioverpa
34	249	19.7	109	6 Q8WMT4	Q8WMT4 bos taurus
35	233	18.4	243	12 Q9JEM1	Q9JEM1 cydia pomon
36	229	18.1	195	13 Q9IA70	Q9IA70 gallus gall
37	229	18.1	197	13 Q9IA69	Q9IA69 gallus gall
38	227.5	18.0	374	11 Q921N0	Q921N0 mus musculu
39	224	17.7	597	11 Q9R015	Q9R015 mus musculu
40	205	16.2	208	12 Q5Y770	Q5Y770 chilo iride
41	200.5	15.9	155	12 Q9YMI9	Q9YMI9 lymantria d
42	197.5	15.6	275	12 Q91ET9	Q91ET9 cydia pomon
43	196.5	15.5	210	4 Q9BOV0	Q9BOV0 homo sapien
44	193.5	15.3	150	12 Q9YVJ4	Q9YVJ4 melanooplus
45	192	15.2	292	12 Q92394	Q92394 bombyx mori

ALIGNMENTS

RESULT 1

ID Q96P09 PRELIMINARY; PRT; 236 AA.
AC Q96P09;
DT 01-DEC-2001 (TREMBLREL. 19, Created)
DT 01-DEC-2001 (TREMBLREL. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLREL. 20, Last annotation update)
DE Testis-specific Inhibitor of Apoptosis.
GN BIRC8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kornejuk R.G., Lagace M.C.;
RT "Genomic Organization of the X-linked Inhibitor of Apoptosis and
RT Identification of a Novel Testis-Specific Transcript."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF420440; AAL30369.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
KW Zinc-finger.
SQ SEQUENCE 236 AA; CB7F034BDDFDAD9D CRC64;

Query Match 100.0%; Score 1264; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.7e-95;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGFEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVCFCGCGGIANKPKEDPWEQHA 60
|||||
DB 1 MTGFEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVCFCGCGGIANKPKEDPWEQHA 60
|||||
QY 61 KWYQCKLLEKGEHYINNIHLTSLDEGALVOTTKRTSLTKRISDTLFPNMQEALR 120

Db	61	KWPCCKYLLEEKGEHYINNIHLTRSLGALVQTTKTSLFKRISDTIFPNMLGPAIR	120
QY	121	MGFDKDYKKIMEEKIQTSNGSKYKILEVYVADIVSAQKTTENELNOTSLQREISPEPL	180
Db	121	MGFDKDYKKIMEEKIQTSNGSKYKILEVYVADIVSAQKTTENELNOTSLQREISPEPL	180
QY	181	RLQDEKJCKICKMDRYIAVVFIPCGHLVYCKCOCAEAVDPCPMCSAVYIDFKORFMS	236
Db	181	RLQDEKJCKICKMDRYIAVVFIPCGHLVYCKCOCAEAVDPCPMCSAVYIDFKORFMS	236

RESULT 2	
Q96RW5	
ID Q96RW5	PRELIMINARY;
AC 006RW5	PRT; 236 AA

DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, last annotation update)
DE IAP-like protein 2.
GN IAP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
RA Mir S.S., Duckett C.S.;
RT "Molecular cloning of human homologs of IAP-like protein."
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
CC CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF164682; AAK81892.1; -
DR InterPro: IPR001370; BIR_ -
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR_1.
DR Pfam: PF00097; zf-C3HC4_1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_1.
DR PROSITE: PS50143; BIR_REPEAT_2; 1.
KW Zinc-finger.
SQ SEQUENCE 236 AA; 27089 MW; DF3A170E0DDFA9D CRC64;

Query Match	99.6%;	Score 1259;	DB 4;	Length 236;
Best Local Similarity	99.6%;	Pred. No. 9.4e-95;		
Matches 235; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	MTGEAALLIFPGTMMASVNNKQOLARAGYALGOEDKVOCCFPGGGGLAMWKPREDEWEOHA	60
Db	1	MTGEAALLIFPGTMMASVNNKQOLARAGYALGOEDKVOCCFPGGGGLAMWKPREDEWEOHA	60
QY	61	KWPGCKYLLDEKGEHEXINNHLIRLSLEGALVQTTKPTSLTKRISDFIFPMPLOEAR	120
Db	61	KWPGCKYLLDEKGEHEXINNHLIRLSLEGALVQTTKPTSLTKRISDFIFPMPLOEAR	120
QY	121	MGDFKVKYKIMEIRIOTSGSNKYTLEVLADVSAOKDTTENELIQTSLQREISPEEPL	180
Db	121	MGDFKVKYKIMEIRIOTSGSNKYTLEVLADVSAOKDTTENELIQTSLQREISPEEPL	180
QY	181	RRLOEKILICIMDRYIAVAVIFPCGHVYTCQCAEADRCMGSAYIDFKQRVENS	236
Db	181	RRLOEKILICIMDRYIAVAVIFPCGHVYTCQCAEADRCMGSAYIDFKQRVENS	236

RESULT 3		
Q95M72		
ID	PRELIMINARY:	PRT, 236 AA.
Q95M72		
AC Q95M72;		
DT 01-DEC-2001 (TREMBLrel. 19	Created)	
DT 01-DEC-2001 (TREMBLrel. 19,	Last sequence update)	
DT 01-MAR-2002 (TREMBLrel. 20,	Last annotation update)	
DE IAP-like protein 2.		
OS Pan troglodytes (Chimpanzee).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.		

```

OX      NCBI_TaxID=9598;
[1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21286921; PubMed=11390657;
RA      Richter B.W.M., Mir S.S., Elden U.J., Lewis J., Refey S.B.,
RA      Frittlin A., Yen L., Frank S., Youle R.J., Nelson D.L.,
RA      Notarangelo U.D., Vezzoni P., Fearhead H.O., Duckett C.S.;
RT      "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT      apoptosis protein family."
RT      Mol. Cell. Biol. 21:4292-4301(2001).
CC      1. SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR      EMBL; AY030052; AAK49776.1; -.
DR      InterPro; IPR001370; BIR.
DR      InterPro; IPR001841; znf_ring.
DR      Pfam; PF00653; BIR. 1.
DR      Pfam; PF00097; zf-C3HC4. 1.
DR      ProSITE; PS01283; BIR_REPEAT_1; UNKNOWN_1.
DR      ProSITE; PS0143; BIR_REPEAT_2; 1.
KW      Zinc-finger
SQ      SEQUENCE 236 AA; 27136 MW; 64CCA3A251420EDE CRC64;..

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Query Match	98.2%	Score 1241;	DB 6;	Length 236;
Best Local Similarity	97.9%	Pred. No. 2.7e-93;		
Matches 231; Conservative	3;	Mismatches 2;	Indels 0;	Gaps 0

QY	1	MTGVEARLITITGTMWY	SYNKEO	LAAGFA	IGOEKVOC	HCGGGI	LANPK	PKEDP	MEQHA	60
Db	1	MTGVEARLITITGTMWY	EVNKEO	LAAGFA	IGOEKVOC	HCGGGI	LANPK	PKEDP	MEQHA	60
QY	61	KWPGCKYLLBEKGHE	YNNI	HLTRSL	EGALVQTT	KKTPTSL	KTRISDT	FTFPNML	OEALR	120
Db	61	KWPGCKYLLBEKGHE	YNNI	HLTRSL	EGALVQTT	KKTPTSL	KTRINDT	FTFPNML	OEALR	120
QY	121	MGFPFKDYKKTMEER	IQTSGS	NYKTL	EVYVAD	LSAQKDT	ENELNQT	SLQREI	SPEEP	180
Db	121	MGFPFKDYKKTMEER	IQTSGS	NYKTL	EVYVAD	LSAQKDT	ENESNQT	SLQREI	SPEEP	180
QY	181	RRLODEERKCKICM	BRYIAV	VPFG	HLVTCQ	CAAVBRC	PMCSAVI	DPKQRE	YMS	236
Db	181	RRLODEERKCKICM	BRYIAV	VPFG	HLVTCQ	CAAVBRC	PMCSAVI	DPKQRE	YMS	236

RESULT 4	
Q95M71	
ID Q95M71	PRELIMINARY;
OC Q95M71	PRT; 236 AA

DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, last annotation update)
DE IAP-like protein 2.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
OX NCBI_TaxID=9593;
OX [1]
RN RP
RP SEQUENCE FROM N.A.
RX MEDLINE=21286921; PubMed=11390657;
RA Richter B.W.M., Mir S.S., Elden L.J., Lewis J., Refey S.B.,
RA Fratini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
RA Notarangelo L.D., Vezoni P., Fearhead H.O., Duckett C.S.,
RT "Molecular cloning of ILP-2, a novel member of the inhibitor of
RT apoptosis protein family.";
RT Mol. Cell. Biol. 21:4292-4301(2001).
RL -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC EMBL; AF030053; AKA49777.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; znf_fing.
DR Pfam; PF00653; BIR. 1.
DR Pfam; PF00097; zf-C3HC4. 1.
DR PROSITE; PSS0143; BIR_REPEAT_2. 1.
KW Zinc-finger.
QZ SEQUENCE 236 AA; 27120 MW; C3A70E39DE442E4C CRC64;

Query Match 97.9%; Score 1237; DB 6; Length 236;
 Best Local Similarity 97.0%; Pred. No. 5, 8e-93;
 Matches 229; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTGEARLITFGTWTWSVKNKEQLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
 DB 1 MTGEARLITFGTWTWSVKNKEQLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
 QY 61 KMYPGCKYLLERKGEHYINNIHLTRSLGALVOTTKTPSLTKRISDTIFPNPMQEAIR 120
 DB 61 KMYPGCKYLLERKGEHYINNIHLTRSLGALVOTTKTPSLTKRISDTIFPNPMQEAIR 120
 QY 121 MGDFDVKKIMEERLOTSSNKTLEVLVADLVSAQKDTENELNOTSLQREISPEEPL 180
 DB 121 MGDFDVKKIMEERLOTSSNKTLEVLVADLVSAQKDTENELNOTSLQREISPEEPL 180
 QY 181 RLQOEKLCIKMDRIYAVFIPCGHLVTCCKCAEAVDRCPMCSAVIDEKORVMS 236
 DB 181 RLQOEKLCIKMDRIYAVFIPCGHLVTCCKCAEAVDRCPMCSAVIDEKORVMS 236

RESULT 5

Q9ESFO PRELIMINARY; PRT; 496 AA.

AC Q9ESFO; 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Inhibitor of apoptosis protein 3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
 RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
 Apoptosis Protein 1, 2, and 3 Genes."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AF183429; AAG22969.1; -.
 DR HSSP; Q13490; 10BH.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 3.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR Zinc-finger.
 SQ SEQUENCE 496 AA; 56117 MW; 9BEF142AEC5B798 CRC64;

Query Match 81.1%; Score 1025; DB 11; Length 496;
 Best Local Similarity 76.6%; Pred. No. 2, 5e-75;
 Matches 180; Conservative 33; Mismatches 22; Indels 0; Gaps 0;

QY 1 MTGEARLITFGTWTWSVKNKEQLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
 DB 1 MTGEARLITFGTWTWSVKNKEQLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
 QY 261 MAEYDARIYFTGTWYTSVKNKEQLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 320
 DB 261 MAEYDARIYFTGTWYTSVKNKEQLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 320
 QY 61 KMYPGCKYLLERKGEHYINNIHLTRSLGALVOTTKTPSLTKRISDTIFPNPMQEAIR 120
 DB 61 KMYPGCKYLLERKGEHYINNIHLTRSLGALVOTTKTPSLTKRISDTIFPNPMQEAIR 120
 QY 321 KMYPGCKYLLERKGEHYINNIHLTRSLGALVOTTKTPSLTKRISDTIFPNPMQEAIR 380
 DB 321 KMYPGCKYLLERKGEHYINNIHLTRSLGALVOTTKTPSLTKRISDTIFPNPMQEAIR 380
 QY 121 MGDFDVKKIMEERLOTSSNKTLEVLVADLVSAQKDTENELNOTSLQREISPEEPL 180
 DB 121 MGDFDVKKIMEERLOTSSNKTLEVLVADLVSAQKDTENELNOTSLQREISPEEPL 180
 QY 381 MGFNFKDIKKTMEERLOTSSNKTLEVLVADLVSAQKDTENELNOTSLQREISPEEPL 440
 DB 381 MGFNFKDIKKTMEERLOTSSNKTLEVLVADLVSAQKDTENELNOTSLQREISPEEPL 440
 QY 181 RLQOEKLCIKMDRIYAVFIPCGHLVTCCKCAEAVDRCPMCSAVIDEKORVMS 235
 DB 441 RLQOEKLCIKMDRIYAVFIPCGHLVTCCKCAEAVDRCPMCSAVIDEKORVMS 495

RESULT 6

Q9EQ05 PRELIMINARY; PRT; 501 AA.

AC Q9EQ05; 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Inhibitor of apoptosis protein 3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
 RT "Cloning, characterization and regulation of an inhibitor of apoptosis
 protein in the rat corpus luteum."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AF304333; AAG41192.1; -.
 DR HSSP; Q13490; 10BH.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 3.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR Zinc-finger.
 SQ SEQUENCE 501 AA; 56548 MW; 0973BF28E81C5A0 CRC64;

Query Match 80.3%; Score 1015; DB 11; Length 501;
 Best Local Similarity 77.2%; Pred. No. 1, 7e-74;
 Matches 179; Conservative 32; Mismatches 21; Indels 0; Gaps 0;

QY 1 MTGEARLITFGTWTWSVKNKEQLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
 DB 1 MTGEARLITFGTWTWSVKNKEQLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 60
 QY 261 MAEYDARIYFTGTWYTSVKNKEQLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 320
 DB 261 MAEYDARIYFTGTWYTSVKNKEQLARAGFYAIGQEDKVCFCGCGGLANMKPKEDPWEQHA 320
 QY 61 KMYPGCKYLLERKGEHYINNIHLTRSLGALVOTTKTPSLTKRISDTIFPNPMQEAIR 120
 DB 61 KMYPGCKYLLERKGEHYINNIHLTRSLGALVOTTKTPSLTKRISDTIFPNPMQEAIR 120
 QY 321 KMYPGCKYLLERKGEHYINNIHLTRSLGALVOTTKTPSLTKRISDTIFPNPMQEAIR 380
 DB 321 KMYPGCKYLLERKGEHYINNIHLTRSLGALVOTTKTPSLTKRISDTIFPNPMQEAIR 380
 QY 121 MGDFDVKKIMEERLOTSSNKTLEVLVADLVSAQKDTENELNOTSLQREISPEEPL 180
 DB 121 MGDFDVKKIMEERLOTSSNKTLEVLVADLVSAQKDTENELNOTSLQREISPEEPL 180
 QY 381 MGFNFKDIKKTMEERLOTSSNKTLEVLVADLVSAQKDTENELNOTSLQREISPEEPL 440
 DB 381 MGFNFKDIKKTMEERLOTSSNKTLEVLVADLVSAQKDTENELNOTSLQREISPEEPL 440
 QY 181 RLQOEKLCIKMDRIYAVFIPCGHLVTCCKCAEAVDRCPMCSAVIDEKORVMS 232
 DB 441 RLQOEKLCIKMDRIYAVFIPCGHLVTCCKCAEAVDRCPMCSAVIDEKORVMS 492

RESULT 7

Q9EQ04 PRELIMINARY; PRT; 501 AA.

AC Q9EQ04; 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Inhibitor of apoptosis protein 3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
 RT "Cloning, characterization and regulation of an inhibitor of apoptosis
 protein in the rat corpus luteum";

Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF304334; AAG41193.1; -.
DR HSP: Q13490; 1QBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF000653; BIR; 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR Zinc-finger.
KM SEQUENCE 501 AA; 56578 MW; 4863P69F2E0C8CD CRC64;

Query Match 80.0%; Score 1011; DB 11; Length 501;
Best Local Similarity 76.7%; Pred. No. 3.5e-74;
Matches 178; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

QY 1 MGYEARLITFGWMSVYNKEQLARAGFYAIGQEDKVOCFHCGGLANMKRPEDPWEQHA 60
DB 261 MAEYDRRIYTFGWISVYNKEQLARAGFYALGEGDKKCFHCGGLTNKPSBEDPWEQHA 320
QY 61 KWPYGCYLLLEKGEHEYNINHLTRSLGALVQTKTPSLTKRISDTFFPNMLQEAIR 120
DB 321 KWPYGCYLLDEKGOEYINNIHLTHSLGESVYRTAEKPPSYTKKIDDTIFQNPVQEAIR 380
QY 121 MGPFDFVKKIMERIQTSGSNKYTLLEVADLVSAOKDTEENELNQTSLQREISPEEP 180
DB 381 MGPFDFVKKIMERIQTSGSNKYTLLEVADLVSAOKDTEENELNQTSLQREISPEEP 440
QY 181 RLRLQEKELCKICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMSAVIDFKOR 232
DB 441 RLRLQEKELCKICMDRNIATFVPCGHLVTCQCAEAVDRCPMSAVIDFKOR 492

RESULT 8
Q8UVE8 PRELIMINARY; PRT; 493 AA.
Q8UVE8:

AC 08UVE8: 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Inhibitor of apoptosis protein 3.
GN IAP3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT Identification of chicken inhibitor of apoptosis protein XIAP
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF451854; AAL47170.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF000653; BIR; 3.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS00089; ZF_RING_2; 1.
SQ SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;

Query Match 53.7%; Score 678.5; DB 13; Length 493;
Best Local Similarity 52.5%; Pred. No. 3.9e-47;
Matches 124; Conservative 43; Mismatches 64; Indels 5; Gaps 3;

QY 1 MGYEARLITFGWMSVYNKEQLARAGFYAIGQEDKVOCFHCGGLANMKRPEDPWEQHA 60

DB 261 MAEYDRRIYTFGWISVYNKEQLARAGFYALGEGDKKCFHCGGLTNKPSBEDPWEQHA 320
QY 61 KWPYGCYLLLEKGEHEYNINHLTRSLGALVQTKTPSLTKRISDTFFPNMLQEAIR 120
DB 321 KWPYGCYLLDEKGOEYINNIHLTHSLGESVYRTAEKPPSYTKKIDDTIFQNPVQEAIR 380
QY 121 MGPFDFVKKIMERIQTSGSNKYTLLEVADLVSAOKDTEENELNQTSLQREISPEEP 179
DB 377 MGPFDFVKKIMERIQTSGSNKYTLLEVADLVSAOKDTEENELNQTSLQREISPEEP 436
QY 180 RLRLQEKELCKICMDRYIAVVFIPCGHLVTCQCAEAVDRCPMSAVIDFKORVEM 235
DB 437 RLRLQEKELCKICAKNDISVILIPCGHLVTCQCAEAVDRCPMSAVIDFKORVEM 492

RESULT 9
Q8UWD2 PRELIMINARY; PRT; 628 AA.
Q8UWD2:

AC 08UWD2: 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE IAP1.
GN Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20373792; PubMed=10917738;
RX Inohara N., Nunez G.;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF442500; AAL33679.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF000653; BIR; 3.
DR Pfam: PF000619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS02009; CARD; 1.
DR PROSITE: PS00089; ZF_RING_2; 1.
SQ SEQUENCE 628 AA; 70098 MW; 5B68CEB6A87C8A95 CRC64;

Query Match 39.4%; Score 497.5; DB 13; Length 628;
Best Local Similarity 30.9%; Pred. No. 2.8e-32;
Matches 108; Conservative 47; Mismatches 77; Indels 117; Gaps 6;

QY 5 EARLITGCTW--MSVYNKEQLARAGFYAIGQEDKVOCFHCGGLANMKRPEDPWEQHA 62
DB 280 EARLITGCTW--MSVYNKEQLARAGFYAIGQEDKVOCFHCGGLANMKRPEDPWEQHA 339
QY 63 YPGCKYLLLEKGEHEYNINHLTRSLGALVQTKTKT-----PSLTKRISDT 108
DB 340 YPGCKYLLLEKGEHEYNINHLTRSLGALVQTKTKT-----PSLTKRISDT 399
QY 109 IFPNPMLQEAIRMGDFDKKIMERIQTSGSNKYTLLEVADLVSAOKDTEENELNQTSL 164
DB 400 IFPNPMLQEAIRMGDFDKKIMERIQTSGSNKYTLLEVADLVSAOKDTEENELNQTSL 459

QY	165	-----	164
Db	460	AEEASDGETFLKHHALSOBLKSQSLMDHLLLENVISOKEYDSTRNCTSVKQOTGOL	519
QY	165	-----LNQTSLOREI-----SP-----EPTLRLOEEK	187
Db	520	IDLVLISKGNAAEVFEFNWIKKNDVYLLRELIQAQTNESAASPQSLDLPMEQJRRQDEER	579
QY	188	LCKICMDRIAYVFIPCGHLNVCCKCAEAVDRPMSAVIDEFORVPMS	236
Db	580	TKVCMDKKEVNIYFIPOGHLVYCKECPASLRKPCICRGWVKGTKEFLS	628
	RESULT 10		
ID	057319	PRELIMINARY;	PRT; 610 AA.
AC	057319;		
DT	01-JUN-1998 (TREMBlrel. 06, Created)		
DT	01-JUN-1998 (TREMBlrel. 06, Last sequence update)		
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)		
DE	Inhibitor of apoptosis PROTEIN 1 (IAP) (inhibitor of T-cell apoptosis IAP1).		
DE	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauroida; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
NCBI_TaxID=9031;			
NCBI_TaxID=9031;			
SEQUENCE FROM N.A.			
RP	STRAIN-WHITE LECHORN; TISSUE-EMBRYONIC FIBROBLAST;		
RC	MEDLINE-98038801; PubMed-9372964;		
RX	You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;		
RA	"ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a		
RT	mediator of the antapoptotic activity of the v-Rel oncoprotein.";		
RL	Mol. Cell. Biol. 17:7328-7341(1997).		
CC	-1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED CELLS.		
CC	-1- SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF THE V-REL-TRANSFORMED CELLS.		
CC	-1- TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS IN TESTIS, BRAIN, AND SKELETAL MUSCLE.		
CC	-1- INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION PROCESS.		
CC	-1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.		
CC	-1- SIMILARITY: MEMBER OF THE IAP FAMILY.		
CC	-1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF APOPTOSIS PROTEIN REPEAT).		
CC	-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.		
DR	EMBL: AF008592; AAB8044.1; --		
DR	HSSP: Q13490; 1Q8H.		
DR	InterPro: IPR001370; BIR.		
DR	InterPro: IPR001315; CARD.		
DR	InterPro: IPR001841; znf_fing.		
DR	Pfam: PF00653; BIR; 3.		
DR	Pfam: PF00619; CARD; 1.		
DR	Pfam: PF00097; zf-C3HC4; 1.		
DR	SMART; SM00238; BIR; 3.		
DR	SMART; SM00114; CARD; 1.		
DR	PROSITE; PS01282; BIR_REPEAT_1; 3.		
DR	PROSITE; PS0143; BIR_REPEAT_2; 3.		
DR	PROSITE; PS0209; CARD; 1.		
DR	Apoptosis; Zinc-finger; Repeat.		
FT	REPEAT 30 97		
FT	REPEAT 176 242		
FT	REPEAT 262 329		
FT	ZN_FING 563 597		
FT	SEQUENCE 610 AA; 68924 MW; ADF47619650844A6 CRC64;		
Query Match	36.8%;	Score 465;	DB 13;
Best Local Similarity	30.3%;	Pred. No. 1.2e-29;	Length 610;

DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50209; CARD; 1.
 DR Zinc-finger.
 KW SEQUENCE 589 AA; 66777 MW; E6812FEE3EA3412 CRC64;

Query Match 35.2%; Score 445; DB 11; Length 589;
 Best Local Similarity 28.8%; Pred. No. 4.8e-28;
 Matches 102; Conservative 49; Mismatches 83; Indels 120; Gaps 7;

QY 1 MTGYEARLITFGWMTS--VNKEOLARAGFYAIGQEDRVOCFHCGGGLANMKPKEDPWEQ 58
 Db 238 MOTHSAKMTSTFLWPSSVLQPEOLASAGFYVVDHNDVRCFCDCGGLRCPEGDDPWIE 297
 QY 59 HAKWPGCKYLLLEKNGHEYNINI-----HLTRSL-----EGALVQTKTKTPSLTKR 104
 Db 298 HAKWPGCKYLLLEKNGHEYNINI-----HLTRSL-----EGALVQTKTKTPSLTKR 104
 QY 105 ISDTIFPN-PMQEAIRMGDFDKVKKIMEERIQTSGSNKYLEVLADLVSAOKDTTEN 163
 Db 356 WEDAVMMNPVVKAAALDMGFSRLVQTVQRIATGENTRTVSIDIVSALLNADEREE 415
 QY 164 E-----LNQTSLORE----- 173
 Db 416 EKERQSEETASGDSLIRKRNALFQOLTCVPIILDDLLEASVLTKEHDIIRKQTIPL 475
 QY 174 ----- 182
 Db 476 QARELIDTLVKNNAASVFNKSLKEVDSTLYEHLFVEKTKMYIPTEDVSGLSLEQLRR 535
 QY 183 LOEKICKICMDRYIAVPIPCGHLVTCQCAEAVDRCPMCSAVIDFKQRYE 234
 Db 536 LOEKICKICMDREYSIVIFPCGHLVTCQCAEAVIDFKQRYE 234

RESULT 15

ID 08UMH2 PRELIMINARY; PRT; 405 AA.

AC 08UMH2.
 DT 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE xlap.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 CX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20373792; PubMed=10917738;
 RA Inohara N., Nunez G.;
 RT "Genes with homology to mammalian apoptosis regulators identified in
 zebrafish."
 RL Cell Death Differ. 7:509-510(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Inohara N., Nunez G.;
 RL EMBL; AF39767; AAL32047.1; -.
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00653; BIR; 3.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00238; BIR; 3.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50089; ZF_RING_2; 1.

SQ SEQUENCE 405 AA; 45564 MW; A366E342D83BECAB CRC64;

Query Match 34.2%; Score 432; DB 13; Length 405;
 Best Local Similarity 36.4%; Pred. No. 3.5e-27;
 Matches 84; Conservative 38; Mismatches 53; Indels 56; Gaps 4;

QY 4 YEARLITFGTWMYSVNKEOLARAGFYAIGQEDRVOCFHCGGGLANMKPKEDPWEQHAHWY 63
 Db 229 FEGRLDSFGRQHPIDPERLARAGFYSTGRQDVCMFCGGGVKAMMPDDPWEEHARHY 288
 QY 64 PGCKYLLLEKNGHEYNINIHLTRSLLEGALVQTKTKTSITRISDTIFPNMLOAIRMGE 123
 Db 289 PGCKYLLLEKNGHEYNINIVQIR-----YKRPQTON-----GF 319
 QY 124 DEKDVKKIMEERIQTSGSNKYLEVLADLVSAOKDTTENELNQTSLQREISPEEPLRL 183
 Db 320 SSHE-----SGSSAQAALIHSSSDMEFEKAE-----PWTELEKL 352
 QY 184 QEKICKICMDRYIAVPIPCGHLVTCQCAEAVDRCPMCSAVIDFKQRYE 234
 Db 353 QEKICKICMDSDISIVIFPCGHLVTCQCAEAVIDFKQRYE 234

Search completed: June 19, 2003, 10:09:31
 Job time : 83 secs

